PROTEIN-PROTEIN INTERACTIONS Between Shigella flexneri polypeptides And Mammalian Polypeptides

PRIORITY

[0001] This application claims priority on the basis of United States Provisional Application No. 60/261,130, filed January 12, 2001, the contents of which are hereby incorporated by reference.

BACKGROUND OF THE INVENTION

[0002] Most biological processes involve specific protein-protein interactions. Protein-protein interactions enable two or more proteins to associate. A large number of non-covalent bonds form between the proteins when two protein surfaces are precisely matched. These bonds account for the specificity of recognition. Thus, protein-protein interactions are involved, for example, in the assembly of enzyme subunits, in antibody-antigen recognition, in the formation of biochemical complexes, in the correct folding of proteins, in the metabolism of proteins, in the transport of proteins, in the localization of proteins, in protein turnover, in first translation modifications, in the core structures of viruses and in signal transduction.

[0003] General methodologies to identify interacting proteins or to study these interactions have been developed. Among these methods are the two-hybrid system originally developed by Fields and co-workers and described, for example, in U.S. Patent Nos. 5,283,173, 5,468,614 and 5,667,973, which are hereby incorporated by reference.

[0004] The earliest and simplest two-hybrid system, which acted as basis for development of other versions, is an *in vivo* assay between two specifically constructed proteins. The first protein, known in the art as the "bait protein" is a chimeric protein which binds to a site on DNA upstream of a reporter gene by means of a DNA-binding domain or BD. Commonly, the binding domain is the DNA-binding domain from either Gal4 or native *E. coli* LexA and the sites placed upstream of the reporter are Gal4 binding sites or LexA operators, respectively.

[0005] The second protein is also a chimeric protein known as the "prey" in the art. This second chimeric protein carries an activation domain or AD. This activation domain is typically derived from Gal4, from VP16 or from B42.

[0006] Besides the two hybrid systems, other improved systems have been developed to detected protein-protein interactions. For example, a two-hybrid plus one system was developed that allows the use of two proteins as bait to screen available cDNA libraries to detect a third partner. This method permits the detection between proteins that are part of a larger protein complex such as the RNA polymerase II holoenzyme and the TFIIH or TFIID complexes. Therefore, this method, in general, permits the detection of ternary complex

formation as well as inhibitors preventing the interaction between the two previously defined fused proteins.

[0007] Another advantage of the two-hybrid plus one system is that it allows or prevents the formation of the transcriptional activator since the third partner can be expressed from a conditional promoter such as the methionine-repressed Met25 promoter which is positively regulated in medium lacking methionine. The presence of the methionine-regulated promoter provides an excellent control to evaluate the activation or inhibition properties the third partner due to its "on" and "off" switch for the formation of the transcriptional activator. The three-hybrid method is described, for example in Tirode et al., *The Journal of Biological Chemistry*, 272, No. 37 pp. 22995-22999 (1997). incorporated herein by reference.

[0008] Besides the two and two-hybrid plus one systems, yet another variant is that described in Vidal et al, *Proc. Natl. Sci. 93* pgs. 10315-10320 called the reverse two- and one-hybrid systems where a collection of molecules can be screened that inhibit a specific protein-protein or protein/DNA interactions, respectively.

[0009] A summary of the available methodologies for detecting protein-protein interactions is described in Vidal and Legrain, *Nucleic Acids Research* Vol. 27, No. 4 pgs.919-929 (1999) and Legrain and Selig, FEBS Letters 480 pgs. 32-36 (2000) which references are incorporated herein by reference.

[0010] However, the above conventionally used approaches and especially the commonly used two-hybrid methods have their drawbacks. For example, it is known in the art that, more often than not, false positives and false negatives exist in the screening method. In fact, a doctrine has been developed in this field for interpreting the results and in common practice an additional technique such as co-immunoprecipitation or gradient sedimentation of the putative interactors from the appropriate cell or tissue type are generally performed. The methods used for interpreting the results are described by Brent and Finley, Jr. in *Ann. Rev. Genet.*, 31 pgs. 663-704 (1997). Thus, the data interpretation is very questionable using the conventional systems.

[0011] One method to overcome the difficulties encountered with the methods in the prior art is described in WO 99/42612, incorporated herein by reference. This method is similar to the two-hybrid system described in the prior art in that it also uses bait and prey polypeptides. However, the difference with this method is that a step of mating at least one first haploid recombinant yeast cell containing the prey polypeptide to be assayed with a second haploid recombinant yeast cell containing the bait polynucleotide is performed. Of course the person skilled in the art would appreciate that either the first recombinant yeast cell also contains at least one detectable reporter gene that is activated by a polypeptide including a transcriptional activation domain.

[0012] The method described in WO 99/42612 permits the screening of more prey polynucleotides with a given bait polynucleotide in a single step than in the prior art systems due to the cell to cell mating strategy between haploid yeast cells. Furthermore, this method is more thorough and reproducible, as well as sensitive. Thus, the presence of false negatives and/or false positives is extremely minimal as compared to the conventional prior art methods.

[0013] The genus Shigella includes four species (major serogroups): S. dysenteriae (Grp. A), S. flexneri (Grp. B), S. boydii (Grp. C) and S. sonnei (Grp. D) as classified in Bergey's Manual for Systematic Bacteriology (N. R. Krieg, ed., pp. 423-427 (1984)). The genera Shigella and Escherichia are phylogenetically closely related. Brenner and others have suggested that the two are more correctly considered sibling species based on DNA/DNA reassociation studies (D. J. Brenner et al., International J. Systematic Bacteriology, 23:1-7 (1973)). These studies showed that Shigella species are on average 80-89% related to E. coli at the DNA level. Also, the degree of relatedness between Shigella species is on average 80-89%.

[0014] The genus *Shigella* is pathogenic in humans; it causes bacillary dysentery at levels of infection of 10 to 100 organisms.

[0015] Shigellosis or bacillary dysentery is a disease that is endemic throughout the world. The disease presents a particularly serious public health problem in tropical regions and developing countries where Shigella dysenteriae and S. flexneri predominate. In industrialized countries, the principal etiologic agent is S. sonnei although sporadic cases of shigellosis are encountered due to S. flexneri, S. boydii and certain entero-invasive Escherichia coli.

[0016] The primary step in the pathogenesis of bacillary dysentery is invasion of the human colonic mucosa by *Shigella* (Labrec, E. H., H. Schneider, T. J. Magnani, and S. B. Formal. 1964. Epithelial cell penetration as an essential step in the pathogenesis of bacillary dysentery. J. Bacteriol. 88:1503). Mucosal invasion encompasses several steps which include penetration of the bacteria into epithelial cells, intracellular multiplication, killing of host cells, and final spreading to adjacent cells and to connective tissue (Formal, S. B., T. L. Hale, and P. J. Sansonetti. 1983. Invasive enteric pathogens. Rev. Infect. Dis. 5:S702, Rout, W. R., S. B. Formal, R. A. Giannella, and G. J. Dammin. 1975. The pathophysiology of Shigella diarrhea in the Rhesus monkey; intestinal transport, morphology and bacteriological studies. Gastroenterology 68:270, Takeuchi, A., H. Spring, E. H. LaBrec, and S. B. Formal. 1965. Experimental acute colitis in the Rhesus monkey following peroral infection with Shigella flexneri. Am. J. Pathol. 52:503, Takeuchi, A. 1967. Electron microscope studies of experimental Salmonella infection. I. Penetration into cells of the intestinal epithelium by Salmonella typhimurium. Am. J. Pathol. 47:1011). The overall process which is usually

limited to the mucosal surface leads to a strong inflammatory reaction which is responsible for abscesses and ulcerations (Labrec, E. H., H. Schneider, T. J. Magnani, and S. B. Formal. 1964. Epithelial cell penetration as an essential step in the pathogenesis of bacillary dysentery. J. Bacteriol. 88:1503., Rout, W. R., S. B. Formal, R. A. Giannella, and G. J. Dammin. 1975. The pathophysiology of Shigella diarrhea in the Rhesus monkey; intestinal transport, morphology and bacteriological studies. Gastroenterology 68:270, Takeuchi, A., H. Spring, E. H. LaBrec, and S. B. Formal. 1965. Experimental acute colitis in the Rhesus monkey following peroral infection with Shigella flexneri. Am. J. Pathol. 52:503).

[0017] Even though dysentery is characteristic of shigellosis, it may be preceded by watery diarrhea. Diarrhea appears to be the result of disturbances in colonic reabsorption and increased jejunal secretion whereas dysentery is a purely colonic process (Kinsey, M. D., S. B. Formal, G. J. Dammin, and R. A. Giannella. 1976. Fluid and electrolyte transport in Rhesus monkeys challenged intraceacally with Shigella flexneri 2a. Infect. Immun. 14:368). These include toxic megacolon, leukemoid reactions and hemolytic-uremic syndrom ("HUS"). The latter is a major cause of mortality from shigellosis in developing areas (Gianantonio, C., H. Vitacco, F. Mendilaharzu, A. Rutty, and J. Mendilaharzu. 1964. The hemolytic-uremic syndrome. J. Pediatr. 64:478, Koster, F., J. Levin, L. Walker, K. S. K. Tung, R. H. Gilman, M. M. Rajaman, M. A. Majid, S. Islam, and R. C. Williams Jr. 1977. Hemolyticuremic syndrome after shigellosis. Relation to endotoxin and circulating immune complexes. N. Engl. J. Med. 298:927).

[0018] The role of Shiga-toxin produced at high level by S. dysenteriae 1 (Conradi, H., 1903. Ueber loshlishe, durch aseptische Autolyse, erhaltene Giftstoffe von Ruhr--un Typhus bazillen. Dtsch. Med. Wochenschr. 29:26) and Shiga-like toxins ("SLT") produced at low level by S. flexneri and S. sonnei (Keusch, G. T., and M. Jacewicz. 1977. The pathogenesis of Shigella diarrhea. VI. Toxin and antitoxin in Shigella flexneri and Shigella sonnei infections in humans. J. Infect. Dis. 135:552) in the four major stages of shigellosis (i.e., invasion of individual epithelial cells, tissue invasion, diarrhea and systemic symptoms) is not well understood. For review see O'Brien and Holmes (O'Brien, A. D., and R. K. Holmes. 1987. Shiga and Shiga-like toxins, Microbiol, Rev. 51;206). Plasmids of 180-220 kilobases ("kb") are essential in all Shigella species for invasion of individual epithelial cells (Rout, W. R., S. B. Formal, R. A. Giannella, and G. J. Dammin. 1975. The pathophysiology of Shigella diarrhea in the Rhesus monkey; intestinal transport, morphology and bacteriological studies. Gastroenterology 68:270, Sansonetti, P. J., D. J. Kopecko, and S. B. Formal. 1981. Shigella sonnei plasmids: evidence that a large plasmid is neceessary for virulence. Infect. Immun. 34:75. Sansonetti, P. J., T. L. Hale, G. I. Dammin, C. Kapper, H. H. Collins Jr., and S. B. Formal, 1983. Alterations in the pathogenesis of Escherichia coli K12 after transfer of plasmids and chromosomal genes from Shigella flexneri. Infect. Immun. 39:1392). This includes entry, intracellular multiplication and early killing of host cells (Clerc, P., A. Ryter, J. Mounier, and P. J. Sansonetti. 1987. Plasmid-mediated early killing of eucaryotic cells by Shigella flexneri as studied by infection of J774 macrophages. Infect. Immun. 55:521, Clerc, P., and P. J. Sansonetti. 1987. Entry of *Shigella flexneri* into HeLa cells: Evidence for directed phagocytosis involving actin polymerization and myosin accumulation. Infect. Immun. 55:2681). The role of Shiga-toxin and SLT at this stage is unclear.

[0019] Recent evidence indicates that Shiga-toxin is cytotoxic for primary cultures of human colonic cells (Moyer, M. P., P. S. Dixon, S. W. Rothman, and J. E. Brown. 1987. Cytotoxicity of Shiga toxin for human colonic and ileal epithelial cells. Infect. Immun. 55:1533). Tissue invasion requires additional chromosomally encoded products among which are smooth lipopolysaccharides ("LPS") (Sansonetti, P. J., T. L. Hale, G. I. Dammin, C. Kapper, H. H. Collins Jr., and S. B. Formal. 1983. Alterations in the pathogenesis of Escherichia coli K12 after transfer of plasmids and chromosomal genes from Shigella flexneri. Infect. Immun. 39:1392), the non-characterized product of the Kcp locus, and aerobactin. A region of the S. flexneri chromosome necessary for fluid production in rabbit ileal loops has been localized to the rha-mt1 regions and near the lysine decarboxylase locus (Sansonetti, P. J., T. L. Hale, G. I. Dammin, C. Kapper, H. H. Collins Jr., and S. B. Formal. 1983. Alterations in the pathogenesis of Escherichia coli K12 after transfer of plasmids and chromosomal genes from Shigella flexneri. Infect. Immun. 39:1392). However, no evidence has been adduced to show that the ability to cause fluid accumulation is due to the SLT of S. flexneri. Thus, the role of Shiga-toxin in causing the systemic complications of shigellosis is still hypothetical. However, Shiga-toxin can mediate vascular damage since capillary lesions observed in HUS resemble those observed in cerebral vessels of animals injected with this toxin (Bridgewater, F. A. I., R. S. Morgan, K. E. K. Rowson, and G. P. Wright, 1955, the neurotoxin of Shigella shigae. Morphological and functional lesions produced in the central nervous system of rabbits. Br. J. Exp. Pathol. 36: 447, Cavanagh, J. B., J. G. Howard, and J. L. Whitby. 1956. The neurotoxin of Shigella shigae. A comparative study of the effects produced in various laboratory animals. Br. J. Exp. Med. 37:272).

[0020] As described before, the genera of *Shigella* and *Escherichia* are phylogenetically closely related. Furthermore, the pathogenesis of enteroinvasive *E. coli* is very similar to that of *Shigella*. In both, dysentery results from invasion of the colonic epithelial cells followed by intracellular multiplication which leads to bloody, mucous discharge with scanty diarrhea.

[0021] Pathogenic *E. coli* serotypes are collectively referred to as Enterovirulent *E. coli* (EVEC) (J. R. Lupski, et al., J. Infectious Diseases, 157:1120-1123 (1988); M. M. Levine, J. Infectious Diseases, 155:377-389 (1987); M. A. Karmali, Clinical Microbiology Reviews, 2:15-38 (1989)). This group includes at least 5 subclasses of *E. coli*, each having a

characteristic pathogenesis pathway resulting in diarrheal disease. The subclasses include Enterotoxigenic *E. coli* (ETEC), Verotoxin-Producing *E. coli* (VTEC), Enteropathogenic *E. coli* (EPEC), Enteroadherent E. coli (EAEC) and Enteroinvasive E. coli (EIEC). The VTEC include Enterohemorrhagic *E. coli* (EHEC) since these produce verotoxins.

[0022] Thus, detection of *Shigella* and EIEC is important in various medical contexts. For example, the presence of either *Shigella* or EIEC in stool samples is indicative of gastroenteritis, and the ability to screen for their presence is useful in treating and controlling that disease. Detection of *Shigella* or EIEC in any possible transmission vehicle such as food is also important to avoid spread of gastroenteritis.

[0023] That is why there is a great need to construct Protein Interaction Map between Shigella polypeptides and human polypeptides in order to understand mechanisms of Shigella pathogenesis and to identify drug target to treat Shigella associated diseases and Shigella detection means.

SUMMARY OF THE PRESENT INVENTION

[0024] Thus, it is an object of the present invention to identify protein-protein interactions between *Shigella* polypeptides and mammalian, preferably human, polypeptides.

[0025] It is another object of the present invention to identify protein-protein interactions between *Shigella* polypeptides and mammalian, preferably human, polypeptides for the development of more effective and better targeted therapeutic applications.

[0026] It is yet another object of the present invention to identify complexes of polypeptides or polynucleotides encoding the polypeptides and fragments of the polypeptides of *Shigella* genus and polypeptides and fragments of the polypeptides of mammals, preferably human.

[0027] It is yet another object of the present invention to identify antibodies to these complexes of polypeptides or polynucleotides encoding the polypeptides and fragments of the polypeptides of *Shigella* genus and mammals, preferably human, including polyclonal, as well as monoclonal antibodies that are used for detection.

[0028] It is still another object of the present invention to identify selected interacting domains of the polypeptides, called SID® polypeptides.

[0029] It is still another object of the present invention to identify selected interacting domains of the polynucleotides, called SID® polynucleotides.

[0030] It is another object of the present invention to generate protein-protein interactions maps called PIM®s.

[0031] It is yet another object of the present invention to provide a method for screening drugs for agents which modulate the interaction of proteins and pharmaceutical compositions that are capable of modulating the protein-protein interactions between Shigella polypeptides and mammalian, preferably human, polypeptides.

[0032] It is another object to administer the nucleic acids of the present invention via gene therapy.

[0033] It is yet another object of the present invention to provide protein chips or protein microarrays.

[0034] It is yet another object of he present invention to provide a report in, for example paper, electronic and/or digital forms, concerning the protein-protein interactions, the modulating compounds and the like as well as a PIM®.

[0035] Thus the present invention, in one aspect thereof, relates to a protein complex between a *Shigella* polypeptide and a mammalian polypeptide. In another embodiment, the Shigella and the mammalian polypeptides are polypeptides set forth on columns 1 and 3 respectively of Table II.

[0036] Furthermore, the present invention provides SID® polynucleotides and SID® polypeptides of Table III, as well as a PIM® between *Shigella* polypeptides and mammalian, preferably human, polypeptides.

[0037] The present invention also provides antibodies to the protein-protein complexes between Shigella polypeptides and mammal, preferably human, polypeptides.

[0038] In another embodiment the present invention provides a method for screening drugs for agents that modulate the protein-protein interactions and pharmaceutical compositions that are capable of modulating protein-protein interactions.

[0039] In another embodiment the present invention provides protein chips or protein microarrays.

[0040] In yet another embodiment the present invention provides a report in, for example, paper, electronic and/or digital forms.

BRIFF DESCRIPTION OF THE DRAWINGS

[0041] Fig. 1 is a schematic representation of the pB1 plasmid.

[0042] Fig. 2 is a schematic representation of the pB5 plasmid.

[0043] Fig. 3 is a schematic representation of the pB6 plasmid.

[0044] Fig. 4 is a schematic representation of the pB13 plasmid.

[0045] Fig. 5 is a schematic representation of the pB14 plasmid.

[0046] Fig. 6 is a schematic representation of the pB20 plasmid.

[0047] Fig. 7 is a schematic representation of the pP1 plasmid.

[0048] Fig. 8 is a schematic representation of the pP2 plasmid.

[0049] Fig. 9 is a schematic representation of the pP3 plasmid.

[0050] Fig. 10 is a schematic representation of the pP6 plasmid.

[0051] Fig. 11 is a schematic representation of the pP7 plasmid.

[0052] Fig. 12 is a schematic representation of vectors expressing the T25 fragment.

[0053] Fig. 13 is a schematic representation of vectors expressing the T18 fragment.

[0054] Fig. 14 is a schematic representation of various vectors of pCmAHL1, pT25 and pT18.

[0055] Fig. 15 is a schematic representation of identification of SID®. In this figure the "Full-length prey protein" is the Open Reading Frame (ORF) or coding sequence (CDS) where the identified prey polypeptides are included. The Selected Interaction Domain (SID®) is determined by the commonly shared polypeptide domain of every selected prey fragment.

[0056] Fig. 16 is a protein map (PIM®).

DETAILED DESCRIPTION OF THE INVENTION

[0057] As used herein the terms "polynucleotides", "nucleic acids" and "oligonucleotides" are used interchangeably and include, but are not limited to RNA, DNA, RNA/DNA sequences of more than one nucleotide in either single chain or duplex form. The polynucleotide sequences of the present invention may be prepared from any known method including, but not limited to, any synthetic method, any recombinant method, any ex vivo generation method and the like, as well as combinations thereof.

[0058] The term "polypeptide" means herein a polymer of amino acids having no specific length. Thus, peptides, oligopeptides and proteins are included in the definition of "polypeptide" and these terms are used interchangeably throughout the specification, as well as in the claims. The term "polypeptide" does not exclude post-translational modifications such as polypeptides having covalent attachment of glycosyl groups, aceteyl groups, phosphate groups, lipid groups and the like. Also encompassed by this definition of "polypeptide" are homologs thereof.

[0059] By the term "homologs" is meant structurally similar genes contained within a given species, orthologs are functionally equivalent genes from a given species or strain, as determined for example, in a standard complementation assay. Thus, a polypeptide of interest can be used not only as a model for identifying similiar genes in given strains, but also to identify homologs and orthologs of the polypeptide of interest in other species. The orthologs, for example, can also be identified in a conventional complementation assay. In addition or alternatively, such orthologs can be expected to exist in bacteria (or other kind of cells) in the same branch of the phylogenic tree, as set forth, for example, at ftp://ftp.cme.msu.edu/pub/rdp/SSU-rRNA/SSU/Prok.phylo.

[0060] As used herein the term "prey polynucleotide" means a chimeric polynucleotide encoding a polypeptide comprising (i) a specific domain; and (ii) a polypeptide that is to be tested for interaction with a bait polypeptide. The specific domain is preferably a transcriptional activating domain.

[0061] As used herein, a "bait polynucleotide" is a chimeric polynucleotide encoding a chimeric polypeptide comprising (i) a complementary domain; and (ii) a polypeptide that is to

be tested for interaction with at least one prey polypeptide. The complementary domain is preferably a DNA-binding domain that recognizes a binding site that is further detected and is contained in the host organism.

[0062] As used herein "complementary domain" is meant a functional constitution of the activity when bait and prey are interacting; for example, enzymatic activity.

[0063] As used herein "specific domain" is meant a functional interacting activation domain that may work through different mechanisms by interacting directly or indirectly through intermediary proteins with RNA polymerase II or III-associated proteins in the vicinity of the transcription start site.

[0064] As used herein the term "complementary" means that, for example, each base of a first polynucleotide is paired with the complementary base of a second polynucleotide whose orientation is reversed. The complementary bases are A and T (or A and U) or C and G.

[0065] The term "sequence identity" refers to the identity between two peptides or between two nucleic acids. Identity between sequences can be determined by comparing a position in each of the sequences which may be aligned for the purposes of comparison. When a position in the compared sequences is occupied by the same base or amino acid, then the sequences are identical at that position. A degree of sequence identity between nucleic acid sequences is a function of the number of identical nucleotides at positions shared by these sequences. A degree of identity between amino acid sequences is a function of the number of identical amino acid sequences that are shared between these sequences. Since two polypeptides may each (i) comprise a sequence (i.e., a portion of a complete polynucleotide sequence) that is similar between two polynucleotides, and (ii) may further comprise a sequence that is divergent between two polynucleotides, sequence identity comparisons between two or more polynucleotides over a "comparison window" refers to the conceptual segment of at least 20 contiguous nucleotide positions wherein a polynucleotide sequence may be compared to a reference nucleotide sequence of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

[0066] To determine the percent identity of two amino acids sequences or two nucleic acid sequences, the sequences are aligned for optimal comparison. For example, gaps can be introduced in the sequence of a first amino acid sequence or a first nucleic acid sequence for optimal alignment with the second amino acid sequence or second nucleic acid sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied

by the same amino acid residue or nucleotide as the corresponding position in the second sequence, the molecules are identical at that position.

[0067] The percent identity between the two sequences is a function of the number of identical positions shared by the sequences. Hence % identity = number of identical positions / total number of overlapping positions X 100.

[0068] In this comparison the sequences can be the same length or may be different in length. Optimal alignment of sequences for determining a comparison window may be conducted by the local homology algorithm of Smith and Waterman (*J. Theor. Biol.*, 91 (2) pgs. 370-380 (1981), by the homology alignment algorithm of Needleman and Wunsch, *J. Miol. Biol.*, 48(3) pgs. 443-453 (1972), by the search for similarity via the method of Pearson and Lipman, *PNAS*, *USA*, 85(5) pgs. 2444-2448 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetic Computer Group, 575, Science Drive, Madison, Wisconsin) or by inspection.

[0069] The best alignment (i.e., resulting in the highest percentage of identity over the comparison window) generated by the various methods is selected.

[0070] The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide by nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size) and multiplying the result by 100 to yield the percentage of sequence identity. The same process can be applied to polypoptide sequences.

[0071] The percentage of sequence identity of a nucleic acid sequence or an amino acid sequence can also be calculated using BLAST software (Version 2.06 of September 1998) with the default or user defined parameter.

[0072] The term "sequence similarity" means that amino acids can be modified while retaining the same function. It is known that amino acids are classified according to the nature of their side groups and some amino acids such as the basic amino acids can be interchanged for one another while their basic function is maintained.

[0073] The term "isolated" as used herein means that a biological material such as a nucleic acid or protein has been removed from its original environment in which it is naturally present. For example, a polynucleotide present in a plant, mammal or animal is present in its natural state and is not considered to be isolated. The same polynucleotide separated

from the adjacent nucleic acid sequences in which it is naturally inserted in the genome of the plant or animal is considered as being "isolated."

[0074] The term "isolated" is not meant to exclude artificial or synthetic mixtures with other compounds, or the presence of impurities which do not interfere with the biological activity and which may be present, for example, due to incomplete purification, addition of stabilizers or mixtures with pharmaceutically acceptable excipients and the like.

[0075] "Isolated polypeptide" or "isolated protein" as used herein means a polypeptide or protein which is substantially free of those compounds that are normally associated with the polypeptide or protein in a naturally state such as other proteins or polypeptides, nucleic acids, carbohydrates, lipids and the like.

[0076] The term "purified" as used herein means at least one order of magnitude of purification is achieved, preferably two or three orders of magnitude, most preferably four or five orders of magnitude of purification of the starting material or of the natural material. Thus, the term "purified" as utilized herein does not mean that the material is 100% purified and thus excludes any other material.

[0077] The term "variants" when referring to, for example, polynucleotides encoding a polypeptide variant of a given reference polypeptide are polynucleotides that differ from the reference polypeptide but generally maintain their functional characteristics of the reference polypeptide. A variant of a polynucleotide may be a naturally occurring allelic variant or it may be a variant that is known naturally not to occur. Such non-naturally occurring variants of the reference polynucleotide can be made by, for example, mutagenesis techniques, including those mutagenesis techniques that are applied to polynucleotides, cells or organisms.

[0078] Generally, differences are limited so that the nucleotide sequences of the reference and variant are closely similar overall and, in many regions identical.

[0079] Variants of polynucleotides according to the present invention include, but are not limited to, nucleotide sequences which are at least 95% identical after alignment to the reference polynucleotide encoding the reference polypeptide. These variants can also have 96%, 97%, 98% and 99.999% sequence identity to the reference polynucleotide.

[0080] Nucleotide changes present in a variant polynucleotide may be silent, which means that these changes do not alter the amino acid sequences encoded by the reference polynucleotide.

[0081] Substitutions, additions and/or deletions can involve one or more nucleic acids. Alterations can produce conservative or non-conservative amino acid substitutions, deletions and/or additions.

[0082] Variants of a prey or a SID® polypeptide encoded by a variant polynucleotide can possess a higher affinity of binding and/or a higher specificity of binding to its protein or

polypeptide counterpart, against which it has been initially selected. In another context, variants can also loose their ability to bind to their protein or polypeptide counterpart.

[0083] By "anabolic pathway" is meant a reaction or series of reactions in a metabolic pathway that synthesize complex molecules from simpler ones, usually requiring the input of energy. An anabolic pathway is the opposite of a catabolic pathway.

[0084] As used herein, a "catabolic pathway" is a series of reactions in a metabolic pathway that break down complex compounds into simpler ones, usually releasing energy in the process. A catabolic pathway is the opposite of an anabolic pathway.

[0085] As used herein, "drug metabolism" is meant the study of how drugs are processed and broken down by the body. Drug metabolism can involve the study of enzymes that break down drugs, the study of how different drugs interact within the body and how diet and other ingested compounds affect the way the body processes drugs.

[0086] As used herein, "metabolism" means the sum of all of the enzyme-catalyzed reactions in living cells that transform organic molecules.

[0087] By "secondary metabolism" is meant pathways producing specialized metabolic products that are not found in every cell.

[0088] As used herein, "SID®" means a Selected Interacting Domain and is identified as follows: for each bait polypeptide screened, selected prey polypeptides are compared. Overlapping fragments in the same ORF or CDS define the selected interacting domain.

[0089] As used herein the term "PIM®" means a protein-protein interaction map. This map is obtained from data acquired from a number of separate screens using different bait polypeptides and is designed to map out all of the interactions between the polypeptides.

[0090] The term "affinity of binding", as used herein, can be defined as the affinity constant Ka when a given SID® polypeptide of the present invention which binds to a polypeptide and is the following mathematical relationship:

[0091] [SID®/polypeptide complex]

[0092] Ka = -----

[0093] [free SID®] [free polypeptide]

[0094] wherein [free SID®], [free polypeptide] and [SID®/polypeptide complex] consist of the concentrations at equilibrium respectively of the free SID® polypeptide, of the free polypeptide onto which the SID® polypeptide binds and of the complex formed between SID® polypeptide and the polypeptide onto which said SID® polypeptide specifically binds.

[0095] The affinity of a SID® polypeptide of the present invention or a variant thereof for its polypeptide counterpart can be assessed, for example, on a BiacoreTM apparatus marketed by Amersham Pharmacia Biotech Company such as described by Szabo et al *Curr*

Opin Struct Biol 5 pgs. 699-705 (1995) and by Edwards and Leartherbarrow, Anal. Biochem 246 pgs. 1-6 (1997).

[0096] As used herein the phrase "at least the same affinity" with respect to the binding affinity between a SID® polypeptide of the present invention to another polypeptide means that the Ka is identical or can be at least two-fold, at least three-fold or at least five fold greater than the Ka value of reference.

[0097] As used herein, the term "modulating compound" means a compound that inhibits or stimulates or can act on another protein which can inhibit or stimulate the protein-protein interaction of a complex of two polypeptides or the protein-protein interaction of two polypeptides.

[0098] More specifically, the present invention comprises complexes of polypeptides or polynucleotides encoding the polypeptides composed of a bait polypeptide, or a bait polynucleotide encoding a bait polypeptide and a prey polypeptide or a prey polynucleotide encoding a prey polypeptide. The prey polypeptide or prey polynucleotide encoding the prey polypeptide is capable of interacting with a bait polypeptide of interest in various hybrid systems.

[0099] As described in the Background of the present invention there are various methods known in the art to identify prey polypeptides that interact with bait polypeptides of interest. These methods, include, but are not limited to, generic two-hybrid systems as described by Fields et al in *Nature*, 340:245-246 (1989) and more specifically in U.S. Patent Nos. 5,283,173, 5,468,614 and 5,667,973, which are hereby incorporated by reference; the reverse two-hybrid system described by Vidal et al, *supra*; the two plus one hybrid method described, for example, in Tirode et al, *supra*; the yeast forward and reverse 'n'-hybrid systems as described in Vidal and Legrain, *supra*; the method described in WO 99/42612; those methods described in Legrain et al *FEBS Letters* 480 pgs. 32-36 (2000) and the like.

[0100] The present invention is not limited to the type of method utilized to detect protein-protein interactions and therefore any method known in the art and variants thereof can be used. It is however better to use the method described in WO 99/42612 or WO 00/66722, both references incorporated herein by reference due to the methods' sensitivity, reproducibility and reliability.

[0101] Protein-protein interactions can also be detected using complementation assays such as those described by Pelletier et al. at http://www.abrf.org/JBT/Articles/JBT0012/jbt0012.html, WO 00/07038 and WO98/34120.

[0102] Although the above methods are described for applications in the yeast system, the present invention is not limited to detecting protein-protein interactions using yeast, but also includes similar methods that can be used in detecting protein-protein interactions in, for example, mammalian systems as described, for example in Takacs et al., *Proc. Natl. Acad.*

Sci., USA, 90 (21):10375-79 (1993) and Vasavada et al., Proc. Natl. Acad. Sci., USA, 88 (23):10686-90 (1991), as well as a bacterial two-hybrid system as described in Karimova et al (1998), WO99/28746, WO 00/66722 and Legrain et al FEBS Letters, 480 pgs. 32-36 (2000).

[0103] The above-described methods are limited to the use of yeast, mammalian cells and *Escherichia coli* cells, the present invention is not limited in this manner. Consequently, mammalian and typically human cells, as well as bacterial, yeast, fungus, insect, nematode and plant cells are encompassed by the present invention and may be transfected by the nucleic acid or recombinant vector as defined herein.

[0104] Examples of suitable cells include, but are not limited to, VERO cells, HELA cells such as ATCC No. CCL2, CHO cell lines such as ATCC No. CCL61, COS cells such as COS-7 cells and ATCC No. CRL 1650 cells, W138, BHK, HepG2, 3T3 such as ATCC No. CRL6361, A549, PC12, K562 cells, 293 cells, Sf9 cells such as ATCC No. CRL1711 and Cv1 cells such as ATCC No. CCL70.

[0105] Other suitable cells that can be used in the present invention include, but are not limited to, prokaryotic host cells strains such as *Escherichia coli*, (e.g., strain DH5- α), *Bacillus subtilis*, *Salmonella typhimurium*, or strains of the genera of *Pseudomonas*, *Streptomyces* and *Staphylococcus*.

[0106] Further suitable cells that can be used in the present invention include yeast cells such as those of Saccharomyces such as Saccharomyces cerevisiae.

[0107] The bait polynucleotide, as well as the prey polynucleotide can be prepared according to the methods known in the art such as those described above in the publications and patents reciting the known method *per se*.

[0108] The bait polynucleotide of the present invention is obtained from *Shigella flexneri* (see Table I). The prey polynucleotide is obtained form a human placenta cDNA or variants thereof and fragments from the genome or transcriptome of human placenta ranging from about 12 to about 5,000, or about 12 to about 10,000 or from about 12 to about 20,000. The prey polynucleotide is then selected, sequenced and identified.

[0109] A human placenta cDNA prey library is prepared from global human placenta and constructed in the specially designed prey vector pP6 as shown in Figure 10 after ligation of suitable linkers such that every cDNA fragment insert is fused to a nucleotide sequence in the vector that encodes the transcription activation domain of a reporter gene. Any transcription activation domain can be used in the present invention. Examples include, but are not limited to, Gal4,YP16, B42, His and the like. Toxic reporter genes, such as CAT^R, CYH2, CYH1, URA3, bacterial and fungi toxins and the like can be used in reverse two-hybrid systems.

[0110] The polypeptides encoded by the nucleotide inserts of the human placenta cDNA prey library thus prepared are termed "prey polypeptides" in the context of the presently described selection method of the prey polynucleotides.

[0111] The bait polynucleotide can be inserted in bait plasmid pB6 or pB20 as illustrated in Figure 3 or 6 respectively. The bait polynucleotide insert is fused to a polynucleotide encoding the binding domain of, for example, the Gal4 DNA binding domain and the shuttle expression vector is used to transform cells. The bait polynucleotides used in the present invention are describes in Table I. As stated above, any cells can be utilized in transforming the bait and prey polynucleotides of the present invention including mammalian cells, bacterial cells, yeast cells, insect cells and the like.

[0112] In an embodiment, the present invention identifies protein-protein interactions in yeast. In using known methods a prey positive clone is identified containing a vector which comprises a nucleic acid insert encoding a prey polypeptide which binds to a bait polypeptide of interest. The method in which protein-protein interactions are identified comprises the following steps:

[0113] mating at least one first haploid recombinant yeast cell clone from a recombinant yeast cell clone library that has been transformed with a plasmid containing the prey polynucleotide to be assayed with a second haploid recombinant yeast cell clone transformed with a plasmid containing a bait polynucleotide encoding for the bait polypeptide;

[0114] cultivating diploid cell clones obtained in step i) on a selective medium; and

[0115] selecting recombinant cell clones which grow on the selective medium.

[0116] This method may further comprise the step of:

[0117] iv) characterizing the prey polynucleotide contained in each recombinant cell clone which is selected in step iii).

[0118] In yet another embodiment of the present invention, in lieu of yeast, Escherichia coli is used in a bacterial two-hybrid system, which encompasses a similar principle to that described above for yeast, but does not involve mating for characterizing the prey polynucleotide.

[0119] In yet another embodiment of the present invention, mammalian cells and a method similar to that described above for yeast for characterizing the prey polynucleotide are used.

[0120] By performing the yeast, bacterial or mammalian two-hybrid system it is possible to identify for one particular bait an interacting prey polypeptide. The prey polypeptide that has been selected by testing the library of preys in a screen using the two-hybrid, two plus one hybrid methods and the like, encodes the polypeptide interacting with the protein of interest.

[0121] The present invention is also directed, in a general aspect, to a complex of polypeptides, polynucleotides encoding the polypeptides composed of a bait polypeptide or bait polynucleotide encoding the bait polypeptide and a prey polypeptide or prey polynucleotide encoding the prey polypeptide capable of interacting with the bait polypeptide of interest. These complexes are identified in Table II, as the bait amino acid sequences and the prey amino acid sequences, as well as the bait and prey nucleic acid sequences.

[0122] In another aspect, the present invention relates to a complex of polynucleotides consisting of a first polynucleotide, or a fragment thereof, encoding a prey polypeptide that interacts with a bait polypeptide and a second polynucleotide or a fragment thereof. This fragment has at least 12 consecutive nucleotides, but can have between 12 and 5,000 consecutive nucleotides, or between 12 and 10,000 consecutive nucleotides or between 12 and 20,000 consecutive nucleotides.

[0123] The polypeptides of column 1 and 3 from Table II according to the present invention and the complexes of these two polypeptides also form part of the present invention. More specifically, the polypeptides of SEQ ID NOS. 1 to 7 are part of the present invention and their complexes with the polypeptides of Column 3, Table II.

[0124] In yet another embodiment, the present invention relates to an isolated complex of at least two polypeptides encoded by two polypucleotides wherein said two polypeptides are associated in the complex by affinity binding and are depicted in columns 1 and 3 of Table II.

[0125] In yet another embodiment, the present invention relates to an isolated complex comprising at least a polypeptide as described in column 1 of Table II and a polypeptide as described in column 3 of Table II. The present invention is not limited to these polypeptide complexes alone but also includes the isolated complex of the two polypeptides in which fragments and/or homologous polypeptides exhibiting at least 95% sequence identity, as well as from 96% sequence identity to 99.999% sequence identity.

[0126] Also encompassed in another embodiment of the present invention is an isolated complex in which SID® of the prey polypeptides encoded by SEQ ID Nos. 15 to 215 in Table III form the isolated complex.

[0127] Besides the isolated complexes described above, nucleic acids coding for a Selected Interacting Domain (SID®) polypeptide or a variant thereof or any of the nucleic acids set forth in Table III can be inserted into an expression vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. Such transcription elements include a regulatory region and a promoter. Thus, the nucleic acid which may encode a marker compound of the present invention is operably linked to a promoter in the expression vector. The expression vector may also include a replication origin.

[0128] A wide variety of host/expression vector combinations are employed in expressing the nucleic acids of the present invention. Useful expression vectors that can be used include, for example, segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include, but are not limited to, derivatives of SV40 and pcDNA and known bacterial plasmids such as col El, pCR1, pBR322, pMal-C2, pET, pGEX as described by Smith et al [need cite 1988], pMB9 and derivatives thereof, plasmids such as RP4, phage DNAs such as the numerous derivatives of phage I such as NM989, as well as other phage DNA such as M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 micron plasmid or derivatives of the 2m plasmid, as well as centomeric and integrative yeast shuttle vectors; vectors useful in eukaryotic cells such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or the expression control sequences; and the like.

[0129] For example in a baculovirus expression system, both non-fusion transfer vectors, such as, but not limited to pVL941 (BamHI cloning site Summers, pVL1393 (BamHI, Smal, Xbal, EcoRI, Nofl, XmalII, BglII and Psfl cloning sites; Invitrogen) pVL1392 (BglII, Psfl, Nofl, XmalII, EcoRI, Xbal, Smal and BamHI cloning site; Summers and Invitrogen) and pBlueBacIII (BamHI, Bgfl, Psfl, Ncol and HindIII cloning site, with blue/white recombinant screening, Invitrogen), and fusion transfer vectors such as, but not limited to, pAc700(BamHI and KpnI cloning sites, in which the BamHI recognition site begins with the initiation codon; Summers), pAc701 and pAc70-2 (same as pAc700, with different reading frames), pAc360 (BamHI cloning site 36 base pairs downstream of a polyhedrin initiation codon; Invitrogen (1951) and pBlueBacHisA, B, C (three different reading frames with BamHI, Bgfl, Psfl, Ncol and HindIII cloning site, an N-terminal peptide for ProBond purification and blue/white recombinant screening of plaques; Invitrogen (220) can be used.

[0130] Mammalian expression vectors contemplated for use in the invention include vectors with inducible promoters, such as the dihydrofolate reductase promoters, any expression vector with a DHFR expression cassette or a DHFR/methotrexate co-amplification vector such as pED (*Pst*I, *Sal*I, SbaI, Smal and *Eco*RI cloning sites, with the vector expressing both the cloned gene and DHFR; Kaufman, 1991). Alternatively a glutamine synthetase/methionine sulfoximine co-amplification vector, such as pEE14 (*HindIII*, *XbaI*, *SmaI*, *SbaI*, *Eco*RI and *BcI* cloning sites in which the vector expresses glutamine synthetase and the cloned gene; Celltech). A vector that directs episomal expression under the control of the Epstein Barr Virus (EBV) or nuclear antigen (EBNA) can be used such as pREP4 (*BamHI*, *SfII*, *XhoI*, *NotI*, *NotI*, *NotI*, *HindIII*, *NheI*, *PvuII* and *KpnI* cloning sites, constitutive RSV-LTR promoter, hygromycin selectable marker; Invitrogen) pCEP4 (*BamHI*, *SfII*, *XhoI*, *NotI*, *NheI*, *HindIII*, *NheI*, *PvuII* and *KpnI* cloning sites, constitutive hCMV

immediate early gene promoter, hygromycin selectable marker; Invitrogen), pMEP4 (Kpnl, Pvul, Nhel, Hindll, Nofl, Xhol, Sfil, BamHI cloning sites, inducible methallothionein IIa gene promoter, hygromycin selectable marker, Invitrogen), pREP8 (BamHI, Xhol, Nofl, Hindlll, Nhel and Kpnl cloning sites, RSV-LTR promoter, histidinol selectable marker; Invitrogen), pREP9 (Kpnl, Nhel, Hindlll, Nofl, Xhol, Sfil, BamHI cloning sites, RSV-LTR promoter, G418 selectable marker; Invitrogen), and pEBVHis (RSV-LTR promoter, hygromycin selectable marker, N-terminal peptide purifiable via ProBond resin and cleaved by enterokinase; Invitrogen).

[0131] Selectable mammalian expression vectors for use in the invention include, but are not limited to, pRc/CMV (*Hind*III, *Bst*XI, *Not*I, *Sba*I and *Apa*I cloning sites, G418 selection, Invitrogen), pRc/RSV (*Hind*II, *Spe*I, *Bst*XI, *Not*I, *Xba*I cloning sites, G418 selection, Invitrogen) and the like. Vaccinia virus mammalian expression vectors (see, for example Kaufman 1991 that can be used in the present invention include, but are not limited to, pSC11 (*Sma*I cloning site, TK- and β-gal selection), pMJ601 (*SaI*I, *Sma*I, *AfI*I, *Nar*I, *Bsp*MII, *Bam*HI, *Apa*I, *Nhe*I, *Sac*II, *Kpn*I and *Hind*III cloning sites; TK- and β-gal selection), pTKgptF1S (*Eco*RI, *Pst*I, *Sal*II, *Acc*I, *Hind*II, *Sba*I, *Bam*HI and *Hpa* cloning sites, TK or XPRT selection) and the like.

[0132] Yeast expression systems that can also be used in the present include, but are not limited to, the non-fusion pYES2 vector (Xbal, Sphl, Shol, Notl, GstXI, EcoRI, BstXI, BamHI, Sacl, Kpnl and HindIII cloning sites, Invitrogen), the fusion pYESHisA, B, C (Xball, Sphl, Shol, Notl, BstXI, EcoRI, BamHI, Sacl, Kpnl and HindIII cloning sites, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), pRS vectors and the like.

[0133] Consequently, mammalian and typically human cells, as well as bacterial, yeast, fungi, insect, nematode and plant cells an used in the present invention and may be transfected by the nucleic acid or recombinant vector as defined herein.

[0134] Examples of suitable cells include, but are not limited to, VERO cells, HELA cells such as ATCC No. CCL2, CHO cell lines such as ATCC No. CCL61, COS cells such as COS-7 cells and ATCC No. CRL 1650 cells, W138, BHK, HepG2, 3T3 such as ATCC No. CRL6361, A549, PC12, K562 cells, 293 cells, Sf9 cells such as ATCC No. CRL1711 and Cv1 cells such as ATCC No. CCL70.

[0135] Other suitable cells that can be used in the present invention include, but are not limited to, prokaryotic host cells strains such as *Escherichia coli*, (e.g., strain DH5- α), *Bacillus subtilis*, *Salmonella typhimurium*, or strains of the genera of *Pseudomonas*, *Streptomyce*s and *Staphylococcus*.

[0136] Further suitable cells that can be used in the present invention include yeast cells such as those of Saccharomyces such as Saccharomyces cerevisiae.

[0137] Besides the specific isolated complexes, as described above, the present invention relates to and also encompasses SID® polynucleotides. As explained above, for each bait polypeptide, several prey polypeptides may be identified by comparing and selecting the intersection of every isolated fragment that are included in the same polypeptide. Thus the SID® polynucleotides of the present invention are represented by the shared nucleic acid sequences of SEQ ID Nos. 15 to 215 encoding the SID® polypeptides of SEQ ID Nos. 216 to 416 in columns 5 and 7 of Table III, respectively.

[0138] The present invention is not limited to the SID® sequences as described in the above paragraph, but also includes fragments of these sequences having at least 12 consecutive nucleic acids, between 12 and 5,000 consecutive nucleic acids and between 12 and 10,000 consecutive nucleic acids and between 12 and 20,000 consecutive nucleic acids, as well as variants thereof. The fragments or variants of the SID® sequences possess at least the same affinity of binding to its protein or polypeptide counterpart, against which it has been initially selected. Moreover this variant and/or fragments of the SID® sequences alternatively can have between 95% and 99.999% sequence identity to its protein or polypeptide counterpart.

[0139] According to the present invention the variants can be created by known mutagenesis techniques either *in vitro* or *in vivo*. Such a variant can be created such that it has altered binding characteristics with respect to the target protein and more specifically that the variant binds the target sequence with either higher or lower affinity.

[0140] Polynucleotides that are complementary to the above sequences which include the polynucleotides of the SID®'s, their fragments, variants and those that have specific sequence identity are also included in the present invention.

[0141] The polynucleotide encoding the SID® polypeptide, fragment or variant thereof can also be inserted into recombinant vectors which are described in detail above.

[0142] The present invention also relates to a composition comprising the abovementioned recombinant vectors containing the SID® polypeptides in Table III, fragments or variants thereof, as well as recombinant host cells transformed by the vectors. The recombinant host cells that can be used in the present invention were discussed in greater detail above.

[0143] The compositions comprising the recombinant vectors can contain physiological acceptable carriers such as diluents, adjuvants, excipients and any vehicle in which this composition can be delivered therapeutically and can include, but is are not limited to sterile liquids such as water and oils.

[0144] In yet another embodiment, the present invention relates to a method of selecting modulating compounds, as well as the modulating molecules or compounds themselves which may be used in a pharmaceutical composition. These modulating compounds may

act as a cofactor, as an inhibitor, as antibodies, as tags, as a competitive inhibitor, as an activator or alternatively have agonistic or antagonistic activity on the protein-protein interactions.

- [0145] The activity of the modulating compound does not necessarily, for example, have to be 100% activation or inhibition. Indeed, even partial activation or inhibition can be achieved that is of pharmaceutical interest.
- [0146] The modulating compound can be selected according to a method which comprises:
- [0147] cultivating a recombinant host cell with a modulating compound on a selective medium and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:
- [0148] wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide having a DNA binding domain;
- [0149] wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide having a transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;
- [0150] selecting said modulating compound which inhibits or permits the growth of said recombinant host cell.
- [0151] Thus, the present invention relates to a modulating compound that inhibits the protein-protein interactions between *Shigella flexneri* polypeptide and human placenta polypeptide of columns 1 and 3 of Table II, respectively. The present invention also relates to a modulating compound that activates the protein-protein interactions between *Shigella flexneri* polypeptide and human placenta polypeptide of columns 1 and 3 of Table II, respectively.
- [0152] In yet another embodiment, the present invention relates to a method of selecting a modulating compound, which modulating compound inhibits the interaction between Shigella flexneri polypeptide and human placenta polypeptide of columns 1 and 3 of Table II, respectively. This method comprises:
- (a) cultivating a recombinant host cell with a modulating compound on a selective medium and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:
- (i) wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide having a first domain of an enzyme;
- (ii) wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide having an enzymatic transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;

- (b) selecting said modulating compound which inhibits or permits the growth of said recombinant host cell.
- [0153] In the two methods described above any toxic reporter gene can be utilized including those reporter genes that can be used for negative selection including the URA3 gene, the CYH1 gene, the CYH2 gene and the like.
- [0154] In yet another embodiment, the present invention provides a kit for screening a modulating compound. This kit comprises a recombinant host cell which comprises a reporter gene the expression of which is toxic for the recombinant host cell. The host cell is transformed with two vectors. The first vector comprises a polynucleotide encoding a first hybrid polypeptide having a DNA binding domain; and a second vector comprises a polynucleotide encoding a second hybrid polypeptide having a transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact.
- [0155] In yet another embodiment a kit is provided for screening a modulating compound by providing a recombinant host cell, as described in the paragraph above, but instead of a DNA binding domain, the first vector comprises a first hybrid polypeptide containing a first domain of a protein. The second vector comprises a second polypeptide containing a second part of a complementary domain of a protein that activates the toxic reporter gene when the first and second hybrid polypeptides interact.
- [0156] In the selection methods described above, the activating domain can be p42 Gal 4, YP16 (HSV) and the DNA-binding domain can be derived from Gal4 or Lex A. The protein or enzyme can be adenylate cyclase, guanylate cyclase, DHFR and the like.
- [0157] Examples of modulating compounds are set forth in Table III.
- [0158] In yet another embodiment, the present invention relates to a pharmaceutical composition comprising the modulating compounds for preventing or treating bacillary dysentery in a human or animal, most preferably in a mammal.
- [0159] This pharmaceutical composition comprises a pharmaceutically acceptable amount of the modulating compound. The pharmaceutically acceptable amount can be estimated from cell culture assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes or encompasses a concentration point or range having the desired effect in an *in vitro* system. This information can thus be used to accurately determine the doses in other mammals, including humans and animals.
- [0160] The therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or in experimental animals. For example, the LD50 (the dose lethal to 50% of the population) as

well as the ED50 (the dose therapeutically effective in 50% of the population) can be determined using methods known in the art. The dose ratio between toxic and therapeutic effects is the therapeutic index which can be expressed as the ratio between LD 50 and ED50 compounds that exhibit high therapeutic indexes.

[0161] The data obtained from the cell culture and animal studies can be used in formulating a range of dosage of such compounds which lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity.

[0162] The pharmaceutical composition can be administered via any route such as locally, orally, systemically, intravenously, intramuscularly, mucosally, using a patch and can be encapsulated in liposomes, microparticles, microcapsules, and the like. The pharmaceutical composition can be embedded in liposomes or even encapsulated.

[0163] Any pharmaceutically acceptable carrier or adjuvant can be used in the pharmaceutical composition. The modulating compound will be preferably in a soluble form combined with a pharmaceutically acceptable carrier. The techniques for formulating and administering these compounds can be found in "Remington's Pharmaceutical Sciences" Mack Publication Co., Easton, PA, latest edition.

[0164] The mode of administration optimum dosages and galenic forms can be determined by the criteria known in the art taken into account the seriousness of the general condition of the mammal, the tolerance of the treatment and the side effects.

[0165] The present invention also relates to a method of treating or preventing bacillary dysentery in a human or mammal in need of such treatment. This method comprises administering to a mammal in need of such treatment a pharmaceutically effective amount of a modulating compound which binds to a targeted Shigella protein. In a preferred embodiment, the modulating compound is a polynucleotide which may be placed under the control of a regulatory sequence which is functional in the mammal or human.

[0166] In yet another embodiment, the present invention relates to a pharmaceutical composition comprising a SID® polypeptide, a fragment or variant thereof. The SID® polypeptide, fragment or variant thereof can be used in a pharmaceutical composition provided that it is endowed with highly specific binding properties to a bait polypeptide of interest.

- [0167] The original properties of the SID® polypeptide or variants thereof interfere with the naturally occurring interaction between a first protein and a second protein within the cells of the organism. Thus, the SID® polypeptide binds specifically to either the first polypeptide or the second polypeptide.
- [0168] Therefore, the SID® polypeptides of the present invention or variants thereof interfere with protein-protein interactions between *Shigella* or *Escherichia* polypeptides or between a mammal polypeptide.
- [0169] Thus, the present invention relates to a pharmaceutical composition comprising a pharmaceutically acceptable amount of a SID® polypeptide or variant thereof, provided that the variant has the above-mentioned two characteristics; i.e., that it is endowed with highly specific binding properties to a bait polypeptide of interest and is devoid of biological activity of the naturally occurring protein.
- [0170] In yet another embodiment, the present invention relates to a pharmaceutical composition comprising a pharmaceutically effective amount of a polynucleotide encoding a SID® polypeptide or a variant thereof wherein the polynucleotide is placed under the control of an appropriate regulatory sequence. Appropriate regulatory sequences that are used are polynucleotide sequences derived from promoter elements and the like.
- [0171] Polynucleotides that can be used in the pharmaceutical composition of the present invention include the nucleotide sequences of SID®s of SEQ ID Nos. 15 to 215.
- [0172] Besides the SID® polypeptides and polynucleotides, the pharmaceutical composition of the present invention can also include a recombinant expression vector comprising the polynucleotide encoding the SID® polypeptide, fragment or variant thereof.
- [0173] The above described pharmaceutical compositions can be administered by any route such as orally, systemically, intravenously, intramuscularly, intradermally, mucosally, encapsulated, using a patch and the like. Any pharmaceutically acceptable carrier or adjuvant can be used in this pharmaceutical composition.
- [0174] The SID® polypeptides as active ingredients will be preferably in a soluble form combined with a pharmaceutically acceptable carrier. The techniques for formulating and administering these compounds can be found in "Remington's Pharmaceutical Sciences" supra.
- [0175] The amount of pharmaceutically acceptable SID® polypeptides can be determined as described above for the modulating compounds using cell culture and animal models.
- [0176] Such compounds can be used in a pharmaceutical composition to treat or prevent bacillary dysentery.
- [0177] Thus, the present invention also relates to a method of preventing or treating bacillary dysentery in a mammal said method comprising the steps of administering to a

mammal in need of such treatment a pharmaceutically effective amount of a recombinant expression vector comprising a polynucleotide encoding a SID® polypeptide which binds to a either to a *Shigella flexneri* protein or to a human placenta protein involved in a protein-protein interaction between a *Shigella flexneri* protein and an human placenta protein. More specifically, the present invention relates to a method of preventing or treating bacillary dysentery in a mammal said method comprising the steps of administering to a mammal in need of such treatment a pharmaceutically effective amount of:

- (1) a SID® polypeptide of SEQ ID Nos. 216 to 416 or a variant thereof which binds to a targeted Shigella flexneri protein or human placenta protein; or
- (2) a SID® polynucleotide encoding a SID® polypeptide of SEQ ID Nos. 15 to 215 or a variant or a fragment thereof wherein said polynucleotide is placed under the control of a regulatory sequence which is functional in said mammal; or
- (3) a recombinant expression vector comprising a polynucleotide encoding a SID® polypeptide which binds either to a *Shigella flexneri* protein or to a human placenta protein involved in a protein-protein interaction between a *Shigella flexneri* protein and an human placenta protein.
- [0178] In another embodiment the present invention nucleic acids comprising a sequence of SEQ ID Nos. 15 to 215 which encodes the protein of sequence SEQ ID Nos. 216 to 416 and/or functional derivatives thereof are administered to modulate complex (from Table II) function by way of gene therapy. Any of the methodologies relating to gene therapy available within the art may be used in the practice of the present invention such as those described by Goldspiel et al *Clin. Pharm.* 12 pgs. 488-505 (1993).
- [0179] Delivery of the therapeutic nucleic acid into a patient may be direct *in vivo* gene therapy (i.e., the patient is directly exposed to the nucleic acid or nucleic acid-containing vector) or indirect *ex vivo* gene therapy (i.e., cells are first transformed with the nucleic acid in vitro and then transplanted into the patient).
- [0180] For example for *in vivo* gene therapy, an expression vector containing the nucleic acid is administered in such a manner that it becomes intracellular; i.e., by infection using a defective or attenuated retroviral or other viral vectors as described, for example in U.S. Patent 4,980,286 or by Robbins et al, Pharmacol. *Ther.*, 80 No. 1 pgs. 35-47 (1998).
- [0181] The various retroviral vectors that are known in the art are such as those described in Miller et al, *Meth. Enzymol.* 217 pgs. 581-599 (1993) which have been modified to delete those retroviral sequences which are not required for packaging of the viral genome and subsequent integration into host cell DNA. Also adenoviral vectors can be used which are advantageous due to their ability to infect non-dividing cells and such high-capacity adenoviral vectors are described in Kochanek, *Human Gene Therapy*, 10, pgs. 2451-2459 (1999). Chimeric viral vectors that can be used are those described by Reynolds

et al, *Molecular Medecine Today*, pgs. 25 –31 (1999). Hybrid vectors can also be used and are described by Jacoby et al, *Gene Therapy*, **4**, pgs. 1282-1283 (1997).

[0182] Direct injection of naked DNA or through the use of microparticle bombardment (e.g., Gene Gun®; Biolistic, Dupont). or by coating it with lipids can also be used in gene therapy. Cell-surface receptors/transfecting agents or through encapsulation in liposomes, microparticles or microcapsules or by administering the nucleic acid in linkage to a peptide which is known to enter the nucleus or by administering it in linkage to a ligand predisposed to receptor-mediated endocytosis (See, Wu & Wu, J. Biol. Chem., 262 pgs. 4429-4432 (1987)) can be used to target cell types which specifically express the receptors of interest.

[0183] In another embodiment a nucleic acid ligand compound may be produced in which the ligand comprises a fusogenic viral peptide designed so as to disrupt endosomes, thus allowing the nucleic acid to avoid subsequent lysosomal degradation. The nucleic acid may be targeted *in vivo* for cell specific endocytosis and expression by targeting a specific receptor such as that described in WO92/06180, WO93/14188 and WO 93/20221. Alternatively the nucleic acid may be introduced intracellularly and incorporated within the host cell genome for expression by homologous recombination. See, Zijlstra et al, *Nature*, 342, pps. 435-428 (1989).

[0184] In ex vivo gene a gene is transferred into cells in vitro using tissue culture and the cells are delivered to the patient by various methods such as injecting subcutaneously, application of the cells into a skin graft and the intravenous injection of recombinant blood cells such as hematopoietic stem or progenitor cells.

[0185] Cells into which a nucleic acid can be introduced for the purposes of gene therapy include, for example, epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes and blood cells. The blood cells that can be used include, for example, T-lymphocytes, B-lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryotcytes, granulocytes, hematopoietic cells or progenitor cells and the like.

[0186] In yet another embodiment the present invention relates to protein chips or protein microarrays. It is well known in the art that microarrays can contain more than 10,000 spots of a protein that can be robotically deposited on a surface of a glass slide or nylon filter. The proteins attach covalently to the slide surface, yet retain their ability to interact with other proteins or small molecules in solution. In some instances the protein samples can be made to adhere to glass slides by coating the slides with an aldehydecontaining reagent that attaches to primary amines. A process for creating microarrays is described, for example by MacBeath and Schreiber in *Science*, Volume 289, Number 5485, pgs, 1760-1763 (2000) or Service, *Science*, Vol, 289, Number 5485 pg. 1673 (2000). An

apparatus for controlling, dispensing and measuring small quantities of fluid is described, for example, in U.S. Patent No. 6,112,605.

[0187] The present invention also provides a record of protein-protein interactions, PIM®'s, SID®'s and any data encompassed in the following Tables. It will be appreciated that this record can be provided in paper or electronic or digital form.

[0188] In order to fully illustrate the present invention and advantages thereof, the following specific examples are given, it being understood that the same are intended only as illustrative and in no way limitative.

EXAMPLES

EXAMPLE 1: Preparation of a collection of random-primed cDNA fragments

1.A. Collection preparation and transformation in Escherichia coli

1.A.1. Random-primed cDNA fragment preparation

[0189] For the human placenta mRNA sample, random-primed cDNA was prepared from 5 μ g of polyA+ mRNA using a TimeSaver cDNA Synthesis Kit (Amersham Pharmacia Biotech) and with 5 μ g of random N9-mers according to the manufacturer's instructions. Following phenolic extraction, the cDNA was precipitated and resuspended in water. The resuspended cDNA was phosphorylated by incubating in the presence of T4 DNA Kinase (Biolabs) and ATP for 30 minutes at 37°C. The resulting phosphorylated cDNA was then purified over a separation column (Chromaspin TE 400, Clontech), according to the manufacturer's protocol.

1.A.2. Ligation of linkers to blunt-ended cDNA

Oligonucleotide HGX931 (5' end phosphorylated) 1 µg/µl and HGX932 1µg/µl.

Sequence of the oligo HGX931: 5'-GGGCCACGAA-3' (SEQ ID NO. 417)

Sequence of the oligo HGX932: 5'-TTCGTGGCCCCTG-3' (SEQ ID NO. 418)

[0190] Linkers were preincubated (5 minutes at 95°C, 10 minutes at 68°C, 15 minutes at 42°C) then cooled down at room temperature and ligated with cDNA fragments at 16°C overnight.

[0191] Linkers were removed on a separation column (Chromaspin TE 400, Clontech), according to the manufacturer's protocol.

1.A.3. Vector preparation

[0192] Plasmid pP6 (see Figure 10) was prepared by replacing the *SpellXhol* fragment of pGAD3S2X with the double-stranded oligonucleotide:

[0193] The pP6 vector was successively digested with *Sti*1 and *Bam*HI restriction enzymes (Biolabs) for 1 hour at 37°C, extracted, precipitated and resuspended in water. Digested plasmid vector backbones were purified on a separation column (Chromaspin TE 400, Clontech), according to the manufacturer's protocol.

1.A.4. Ligation between vector and insert of cDNA

[0194] The prepared vector was ligated overnight at 15°C with the blunt-ended cDNA described in section 2 using T4 DNA ligase (Biolabs). The DNA was then precipitated and resuspended in water.

1.A.5. Library transformation in Escherichia coli

[0195] The DNA from section 1.A.4 was transformed into Electromax DH10B electrocompetent cells (Gibco BRL) with a Cell Porator apparatus (Gibco BRL). 1 ml SOC medium was added and the transformed cells were incubated at 37°C for 1 hour. 9 mls of SOC medium per tube was added and the cells were plated on LB+ampicillin medium. The colonies were scraped with liquid LB medium, aliquoted and frozen at -80°C.

- [0196] The obtained collection of recombinant cell clones is named HGXBPLARP1.
- 1.B. Collection transformation in Saccharomyces cerevisiae

[0197] The Saccharomyces cerevisiae strain (Y187 (MAT α Gal4 Δ Gal80 Δ ade2-101, his3, leu2-3, -112, trp1-901, ura3-52 URA3::UASGAL1-LacZ Met)) was transformed with the cDNA library.

[0198] The plasmid DNA contained in E. coli were extracted (Qiagen) from aliquoted E. coli frozen cells (1.A.5.). Saccharomyces cerevisiae yeast Y187 in YPGlu were grown.

[0199] Yeast transformation was performed according to standard protocol (Giest et al. Yeast, 11, 355-360, 1995) using yeast carrier DNA (Clontech). This experiment leads to 10^4 to 5×10^4 cells/ μg DNA. 2×10^4 cells were spread on DO-Leu medium per plate. The cells were aliquoted into vials containing 1 ml of cells and frozen at -80°C.

[0200] The obtained collection of recombinant cell clones is named HGXYPLARP1 (placenta).

1.C. Construction of bait plasmids

[0201] For fusions of the bait protein (listed in Table II) to the DNA-binding domain of the GAL4 protein of *S. cerevisiae*, bait fragments were cloned into plasmid pB6. For fusions of the bait protein to the DNA-binding domain of the LexA protein of *E. coli*, bait fragments were cloned into plasmid pB20.

[0202] Plasmid pB6 (see Figure 3) was prepared by replacing the *Nco1/Sal*¹ polylinker fragment of pAS∆∆ with the double-stranded DNA fragment:

5'

[0203] Plasmid pB20 (see Figure 6) was prepared by replacing the *EcoRIPstl* polylinker fragment of pLex10 with the double-stranded DNA fragment:

5'

3'

[0204] The amplification of the bait ORF was obtained by PCR using the Pfu proofreading *Taq* polymerase (Stratagene), 10 pmol of each specific amplification primer and 200 ng of plasmid DNA as template.

[0205] The PCR program was set up as follows :

[0206] The amplification was checked by agarose gel electrophoresis.

[0207] The PCR fragments were purified with Qiaquick column (Qiagen) according to the manufacturer's protocol.

[0208] Purified PCR fragments were digested with adequate restriction enzymes. The PCR fragments were purified with Qiaquick column (Qiagen) according to the manufacturer's protocol.

[0209] The digested PCR fragments were ligated into an adequately digested and dephosphorylated bait vector (pB6 or pB20) according to standard protocol (Sambrook et al.) and were transformed into competent bacterial cells. The cells were grown, the DNA extracted and the plasmid was sequenced.

Example 2: Screening the collection with the two-hybrid in yeast system

2.A. The mating protocol

[0210] The mating two-hybrid in yeast system (as described by Legrain et al., Nature Genetics, vol. 16, 277-282 (1997), Toward a functional analysis of the yeast genome through

exhaustive two-hybrid screens) was used for its advantages but one could also screen the cDNA collection in classical two-hybrid system as described in Fields et al. or in a yeast reverse two-hybrid system.

[0211] The mating procedure allows a direct selection on selective plates because the two fusion proteins are already produced in the parental cells. No replica plating is required.

[0212] This protocol was written for the use of the library transformed into the Y187 strain.

[0213] For bait proteins fused to the DNA-binding domain of GAL4, bait-encoding plasmids were first transformed into *S. cerevisiae* (CG1945 strain (MATa Gal4-542 Gal180-538 ade2-101 his3\(\text{A}\)200, leu2-3\(\text{,112}\), trp1-901, ura3-52, lys2-801, URA3::GAL4 17mers (X3)-CyC1TATA-LacZ, LYS2::GAL1UAS-GAL1TATA-HIS3 CYH^R)) according to step 1.B. and spread on DO-Tro medium.

[0214] For bait proteins fused to the DNA-binding domain of LexA, bait-encoding plasmids were first transformed into *S. cerevisiae* (L40∆gal4 strain (MATa ade2, trp1-901, leu2 3,112, lys2-801, his3∆200, LYS2::(lexAop)₄-HIS3, ura3-52::URA3 (lexAop)₈-LacZ, GAL4::Kan⁶)) according to step 1.B. and spread on DO-Trp medium.

Day 1, morning: preculture

[0215] The cells carrying the bait plasmid obtained at step 1.C. were precultured in 20 ml DO-Trp medium and grown at 30°C with vigorous agitation.

Day 1, late afternoon : culture

[0216] The OD_{600nm} of the DO-Trp pre-culture of cells carrying the bait plasmid preculture was measured. The OD_{600nm} must lie between 0.1 and 0.5 in order to correspond to a linear measurement.50 ml DO-Trp at OD_{600nm} 0.006/ml was inoculated and grown overnight at 30°C with vigorous aditation.

Day 2 : mating medium and plates

1 YPGlu 15cm plate

50 ml tube with 13 ml DO-Leu-Trp-His

100 ml flask with 5 ml of YPGlu

8 DO-Leu-Trp-His plates

2 DO-Leu plates

2 DO-Trp plates

2 DO-Leu-Trp plates

[0217] The OD $_{600nm}$ of the DO-Trp culture was measured. It should be around 1.

[0218] For the mating, twice as many bait cells as library cells were used. To get a good mating efficiency, one must collect the cells at 10° cells per cm².

[0219] The amount of bait culture (in ml) that makes up 50 OD_{600nm} units for the mating with the prev library was estimated.

[0220] A vial containing the HGXYCDNA1 library was thawed slowly on ice. 1.0ml of the vial was added to 5 ml YPGlu. Those cells were recovered at 30°C, under gentle agitation for 10 minutes.

Mating

[0221] The 50 OD_{600nm} units of bait culture was placed into a 50 ml falcon tube.

[0222] The HGXYCDNA1 library culture was added to the bait culture, then centrifuged, the supernatant discarded and resuspended in 1.6ml YPGlu medium.

[0223] The cells were distributed onto two 15cm YPGlu plates with glass beads. The cells were spread by shaking the plates. The plate cells-up at 30°C for 4h30min were incubated.

Collection of mated cells

[0224] The plates were washed and rinsed with 6ml and 7ml respectively of DO-Leu-Trp-His. Two parallel serial ten-fold dilutions were performed in 500µl DO-Leu-Trp-His up to 1/10,000. 50µl of each 1/10000 dilution was spread onto DO-Leu and DO-trp plates and 50µl of each 1/1000 dilution onto DO-Leu-Trp plates. 22.4ml of collected cells were spread in 400µl aliquots on DO-Leu-Trp-His+Tet plates.

Day 4

[0225] Clones that were able to grow on DO-Leu-Trp-His+Tetracyclin were then selected. This medium allows one to isolate diploid clones presenting an interaction.

[0226] The His+ colonies were counted on control plates.

[0227] The number of His+ cell clones will define which protocol is to be processed:

[0228] Upon 60.106 Trp+Leu+ colonies :

- if the number His+ cell clones <285 : then use the process luminometry protocol on all colonies
- if the number of His+ cell clones > 285 and <5000: then process via overlay and then luminometry protocols on blue colonies (2.B and 2.C).
- if number of His+ cell clones >5000 : repeat screen using DO-Leu-Trp-His+Tetracyclin plates containing 3-aminotriazol.

2.B. The X-Gal overlay assay

[0229] The X-Gal overlay assay was performed directly on the selective medium plates after scoring the number of His* colonies.

Materials

[0230] A waterbath was set up. The water temperature should be 50°C.

0.5 M Na₂HPO₄ pH 7.5.

1.2% Bacto-agar.

2% X-Gal in DMF.

Overlay mixture: 0.25 M Na₂HPO₄ pH7.5, 0.5% agar, 0.1% SDS, 7% DMF (LABOSI), 0.04% X-Gal (ICN). For each plate, 10 ml overlay mixture are needed.

DO-Leu-Trp-His plates.

Sterile toothpicks.

Experiment

[0231] The temperature of the overlay mix should be between 45°C and 50°C. The overlay-mix was poured over the plates in portions of 10 ml. When the top layer was settled, they were collected. The plates were incubated overlay-up at 30°C and the time was noted. Blue colonies were checked for regularly. If no blue colony appeared, overnight incubation was performed. Using a pen the number of positives was marked. The positives colonies were streaked on fresh DO-Leu-Trp-His plates with a sterile toothpick.

2.C. The luminometry assay

[0232] His+ colonies were grown overnight at 30°C in microtiter plates containing DO-Leu-Trp-His+Tetracyclin medium with shaking. The day after, the overnight culture was diluted 15 times into a new microtiter plate containing the same medium and was incubated for 5 hours at 30°C with shaking. The samples were diluted 5 times and read OD_{600nm}. The samples were diluted again to obtain between 10,000 and 75,000 yeast cells/well in 100 µl final volume.

[0233] Per well, $76 \,\mu$ l of One Step Yeast Lysis Buffer (Tropix) was added, $20 \,\mu$ l Sapphirell Enhancer (Tropix), $4 \,\mu$ l Galacton Star (Tropix) and incubated 40 minutes at 30°C. The β -Gal read-out (L) was measured using a Luminometer (Trilux, Wallach). The value of $(OD_{PR0000} \times L)$ was calculated and interacting prevs having the highest values were selected.

[0234] At this step of the protocol, diploid cell clones presenting interaction were isolated. The next step was now to identify polypeptides involved in the selected interactions. Example 3: Identification of positive clones

3.A. PCR on yeast colonies

Introduction

[0235] PCR amplification of fragments of plasmid DNA directly on yeast colonies is a quick and efficient procedure to identify sequences cloned into this plasmid. It is directly derived from

[0236] a published protocol (Wang H. et al., Analytical Biochemistry, 237, 145-146, (1996)). However, it is not a standardized protocol and it varies from strain to strain and it is dependent of experimental conditions (number of cells, *Taq* polymerase source, etc). This protocol should be optimized to specific local conditions.

Materials

[0237] For 1 well, PCR mix composition was :

32.5 µl water,

5 µl 10X PCR buffer (Pharmacia),

1 µl dNTP 10 mM.

0.5 μl Taq polymerase (5u/μl) (Pharmacia),

 $0.5\,\mu$ l oligonucleotide ABS1 10 pmole/ μ l: 5'-GCGTTTGGAATCACTACAGG-3',(SEQ ID NO. 424)

 $0.5~\mu l$ oligonucleotide ABS2 10 pmole/ μl : 5'-CACGATGCACGTTGAAGTG-3'.(SEQ ID NO. 425)

1 N NaOH.

Experiment

[0238] The positive colonies were grown overnight at 30°C on a 96 well cell culture cluster (Costar), containing 150 μ l DO-Leu-Trp-His+Tetracyclin with shaking. The culture was resuspended and 100 μ l was transferred immediately on a Thermowell 96 (Costar) and centrifuged for 5 minutes at 4,000 rpm at room temperature. The supernatant was removed. 5 μ l NaOH was added to each well and shaken for 1 minute.

[0239] The Thermowell was placed in the thermocycler (GeneAmp 9700, Perkin Elmer) for 5 minutes at 99.9°C and then 10 minutes at 4°C. In each well, the PCR mix was added and shaken well.

[0240] The PCR program was set up as followed:

94°C 3 minutes
94°C 30 seconds
53°C 1 minute 30 seconds
72°C 3 minutes
72°C 5 minutes

x 35 cycles

[0241] The quality, the quantity and the length of the PCR fragment was checked on an agarose gel. The length of the cloned fragment was the estimated length of the PCR fragment minus 300 base pairs that corresponded to the amplified flanking plasmid sequences.

[0242] 3.B. Plasmids rescue from yeast by electroporation

Introduction

15°C

[0243] The previous protocol of PCR on yeast cell may not be successful, in such a case, plasmids from yeast by electroporation can be rescued. This experiment allows the recovery of prey plasmids from yeast cells by transformation of *E. coli* with a yeast cellular extract. The prey plasmid can then be amplified and the cloned fragment can be sequenced.

[0244] Plasmid rescue

Glass beads 425-600 µm (Sigma)Phenol/chloroform (1/1) premixed with isoamyl alcohol (Amresco)

Extraction buffer: 2% Triton X100, 1% SDS, 100 mM NaCl, 10 mM TrisHCl pH 8.0, 1 mM

EDTA pH 8.0. Mix ethanol/NH₄Ac: 6 volumes ethanol with 7.5 M NH₄ Acetate, 70% Ethanol and yeast cells

in patches on plates.

Electroporation

SOC medium

M9 medium

Selective plates: M9-Leu+Ampicillin

2 mm electroporation cuvettes (Eurogentech)

Experiment

Plasmid rescue

[0245] The cell patch on DO-Leu-Trp-His was prepared with the cell culture of section 2.C. The cell of each patch was scraped into an Eppendorf tube, 300 μl of glass beads was added in each tube, then, 200 μl extraction buffer and 200 μl phenol:chloroform:isoamyl alcohol (25:24:1) was added.

[0246] The tubes were centrifuged for 10 minutes at 15,000 rpm.

[0247] 180 μ l supernatant was transferred to a sterile Eppendorf tube and 500 μ l each of ethanol/NH₄Ac was added and the tubes were vortexed. The tubes were centrifuged for 15 minutes at 15,000 rpm at 4°C. The pellet was washed with 200 µl 70% ethanol and the ethanol was removed and the pellet was dried. The pellet was resuspended in 10 μ l water. Extracts were stored at -20°C.

Flectroporation

Materials:

[0248] Electrocompetent MC1066 cells prepared according to standard protocols (Sambrook et al. supra).

1 µl of yeast plasmid DNA-extract was added to a pre-chilled Eppendorf tube, and kept on ice.

1 μl plasmid yeast DNA-extract sample was mixed and 20 μl electrocompetent cells was added and transferred in a cold electroporation cuvette. Set the Biorad electroporator on 200 ohms resistance, 25 μF capacity; 2.5 kV. Place the cuvette in the cuvette holder and electroporate.

1 ml of SOC was added into the cuvette and the cell-mix was transferred into a sterile Eppendorf tube. The cells were recovered for 30 minutes at 37°C, then spun down for 1 minute at $4,000 \times g$ and the supernatant was poured off. About $100 \mu l$ medium was kept and used to resuspend the cells and spread them on selective plates (e.g., M9-Leu plates). The plates were then incubated for 36 hours at 37° C.

[0249] One colony was grown and the plasmids were extracted. Check for the presence and size of the insert through enzymatic digestion and agarose gel electrophoresis. The insert was then sequenced.

Example 4: Protein-protein interaction

[0250] For each bait, the previous protocol leads to the identification of prey polynucleotide sequences. Using a suitable software program (e.g., Blastwun, available on the Internet site of the University of Washington : http://bioweb.pasteur.fr/seqanal/interfaces/blastwu.html) the identity of the mRNA transcript that is encoded by the prey fragment may be determined and whether the fusion protein encoded is in the same open reading frame of translation as the predicted protein or not.

[0251] Alternatively, prey nucleotide sequences can be compared with one another and those which share identity over a significant region (60nt) can be grouped together to form a contiguous sequence (Contig) whose identity can be ascertained in the same manner as for individual prey fragments described above.

Example 5: Identification of SID®

[0252] By comparing and selecting the intersection of all isolated fragments that are included in the same polypeptide, one can define the Selected Interacting Domain (SID®) as illustrated in Figure 15. The SID® is illustrated in Table III.

Example 6: Identification of PIM®

[0253] The PIM® is then constructed using methods known in the art as exemplified in Figure 16.

Example 7: Making of polyclonal and monoclonal antibodies

[0254] The protein-protein complex of columns 1 and 3 of Table II was injected into mice and polyclonal and monoclonal antibodies were made following the procedure set forth in Sambrook et al. (*supra*).

[0255] More specifically, mice are immunized with an immunogen comprising Table II complexes conjugated to keyhole limpet hemocyanin using glutaraldehyde or EDC as is well known in the art. The complexes can also be stabilized by crosslinking as described in WO 00/37483. The immunogen is then mixed with an adjuvant. Each mouse receives four injections of 10 ug to 100 ug of immunogen, and after the fourth injection, blood samples are taken from the mice to determine if the serum contains antibodies to the immunogen. Serum titer is determined by ELISA or RIA. Mice with sera indicating the presence of antibody to the immunogen are selected for hybridoma production.

[0256] Spleens are removed from immune mice and single-cell suspension is prepared (Harlow et al 1988). Cell fusions are performed essentially as described by Kohler et al (1976). Briefly, P365.3 myeloma cells (ATTC Rockville, Md) or NS-1 myeloma cells are fused with spleen cells using polyethylene glycol as described by Harlow et al (1989). Cells are plated at a density of 2 x 10⁵ cells/well in 96-well tissue culture plates. Individual wells are examined for growth and the supernatants of wells with growth are tested for the presence of the complex-specific antibodies by ELISA or RIA using one of the proteins set forth in Table II as a target protein. Cells in positive wells are expanded and subcloned to establish and confirm monoclonality.

[0257] Clones with the desired specificities are expanded and grown as ascites in mice or in a hollow fiber system to produce sufficient quantities of antibodies for characterization and assay development. Antibodies are tested for binding to one of the proteins in Table II, to determine which are specific for the Table II complexes as opposed to those that bind to the individual proteins. More specifically, antibodies are tested for binding to balt polypeptide of column 1 of Table II alone or to prey polypeptide of column 3 of Table II alone, to determine which are specific for the protein-protein complex of columns 1 and 3 of Table II as opposed to those that bind to the individual proteins.

[0258] Monoclonal antibodies against each of the complexes set forth in columns 1 and 3 of Table II are prepared in a similar manner by mixing specified proteins together, immunizing an animal, fusing spleen cells with myeloma cells and isolating clones which produce antibodies specific for he protein complex, but not for individual proteins.

Example 8: Modulating compounds/PIM screening

[0259] Each specific protein-protein complex of columns 1 and 3 of Table II may be used to screen for modulating compounds.

- [0260] One appropriate construction for this modulating compound screening may be:
- bait polynucleotide inserted in pB6 or pB20;- prey polynucleotide inserted in pP6:
- transformation of these two vectors in a permeable yeast cell;
- growth of the transformed yeast cell on medium containing compound to be tested;
- and observation of the growth of the yeast cells.

[0261] The following results obtained from these Examples, as well as the teachings in the specification are set forth in the Tables below.

[0262] While the invention has been described in terms of the various preferred embodiments, the skilled artisan will appreciate that various modifications, substitutions, omissions and changes may be made without departing from the scope thereof. Accordingly, it is intended that the present invention be limited by the scope of the following claims, including equivalents thereof.

[0263] All patent and non-patent publications cited in this specification, including the websites set forth onpages 8, 13 and 33, are indicative of the level of skill of those skilled in the art to which this invention pertains. All these publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated herein by reference.

IOOHSHB7 GIIIOE

		4:	ö	O. Dillio and codesing
Bait 2: 3: ne Nucle ic acid	3: Nucleic acid sequence	Nucleic Position s		
O	[1-888]	11-888]	8	MNLDGVRPYCRIVNKKNESIS
_	ATGAATTTAGATGTGTTAGACCA/ACIGIAGAAIAGICAAIAAAAATTCATGTAGTGACGCAAAAGCAGCATG			DIAFAHIIKRVKNSSCTHPKAAL
	ATTGCATTTGCACATALAAAAAGAGAAAAAAAAAAAAAAA			VFLGEKGFCDSNDVLSIMGQQ
	GTTTTTTAGGAGAGAGAAAGGIIIIIGIGAIAGCAAIGAIGIIOINGIAAAAAAAAAAAATAAAAATAAAAATAAAAATAAAAATAAAA			IPRVFKNKMLYDYVFKNEKSK
	CCAAGAGTATTTAAGAACAAGATGTTATATGATTAACCAATAATTAAT			NDFLKMAESWLPQSEPIVINN
	TTCTAAAAATGGGIGAAICAIGGGIACCAAAAAAAAAAAA			DDDALNAAAYFSVKKAKIKTV
	GCATTGAAIGCIGCIGCIIALIIIIIIIIIAAAAAAAAAAAAAAA			NDTDFKEYNKVYILGHGSPGS
	TTTAAAGAGTATAATAAGGIIIAIAH			HOLGLGSELIDVQTIISRMKDC
	GGTTCGGAACITALIGALGIACAAACAALCAALAAAAAAAAAAAAAAAAAAA			GILNVKDIRFTSCGSADKVAPK
	AAAGATATCCGTTTTACTICALGCGGCICCGCICALAAAGIGGCICCICAAAAGAATCTTTGCT			NFNNAPAESLSCILNSLPFFKE
	CCTGCTGAAAGTCTTTCTTGTAACTCAAAAAATATCCGGCT			KESLLEQIKKHLENDESLSDGI
	AGAGCAGATAAAAAAACACCIIIGAAAAACGAIGAAIGAAIGAAAAAAAA			KISGYHGYGVHYGQELFPYSH
	ATCATGGATATGGAGTTCACTATGGTCAAGAGCIIIIIICCCIACIACAAAGACTTTTATTATTAATAAAG			YRSTSIPADPEHTVKRSSQKK
	TTCCTGCTGATCCGGAGCALACAGTACAGAGAGCTCTCAGAAAAAAAAAA			TFIINKELD*YKIFNL*
	AACTGGATTAGTATAAAATITITAACCIA AG	[1-711]	6	MSINNYGLHPANNKNMHLIIGS
0	ATGTCAATAAATAACTATGGATTACATCAAAAAAAAAAA			NTANENKGMKNNIINVTNTAIS
	AATACTGCTAATGAAAAA TAAAAAAAAAAAAAAAAAAA			HAINEEKSGGGYSGVSFRKLA
	CACGCCATCAATGAAGAAAAA			KIQNISIPTKNNKEYNRHNLFS
	AAATACAGAACATATCCA1 CCGACAAAGAATAATAAGAAATAATAGATGATTAGAAGAAT			LIWHGNADAARKYSESLLAAE
	TGATTTGGCATGGAAATGCCGATGGCAGCGCGTAAATAAA			PKEEKLEVLAARNNAGESALFI
	ACCCAAAGAGGAAAAACTAGAAGIICIIGCAGCACGAAAIAAIGGGAGATTTATTATTAATTAATTGATT			ALQEGHSAAIQAYGDFIKTFDL
	TAGCICI I CAGAGAGAI CAGATTACTATTACATATATATATAGAGAGTTACAGAGATTATTA			SPKETIKLLDVRDNEGLPGLFL
	TATCACCAAAAGAAACAAACAAAAAAAAAAAAAAAAAAA			AAGKGNIEAMMAYINICHHSGI
	CTGGCCGCAGGGAAAGGGGAAATATATATATATATATATA			KLTEIADRLNNNEODMFNIISD
	GGATAAAACI I ACAGAAAI TACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			KIQELF*VC*IAAKNCT*
	CTGACAAAATACAAGAGIIGIIIIIAAGIIGIGIGIGIGIGIGIGIGIGI	[1-1434]	10	MNISETLNSANTOCNIDSMDN
e e	A I GAATATATATATATATATATATATATATATATATATATA			RLHTLFPKVTSVHNAAQQIMP
	ACA AC			DEKNIKUSANIIKUFFRKIIAA
	AAAAAA I I AAAAAGAH I AAAAAA AAAAAAAAAAA	_	_	QSYSRMFSQGSNFKSLNIAID
	Ald Add Add Color Oversion Color			APSDAKASFKAIEHLUHLSKHY
	GACGCI AAAGCTTCATCTTTTTTTTTTTTTTTTTTTTTTTTTTTT			ISEIREKLHPLSAEELNLLSLIIN
	A LONG TO THE TOTAL OF THE TOTAL THE THE TOTAL			SULIFIED CONSTRUCTION

IDD43487 DIIIIO

AATAAAATTOGGTGTGAAGGAATTIGGACGAAAGGGAAACACCATAGAAAAAAAAATAAAAAAATAAAAAAAA	NIKIOSEGICTKBNTVADDIKKIA					_										ACCAACGGT [1-1005] 11 MINITILINSISTISSISTININING									TATCTCAAAA					TATGGAAATT [1-1149] 12 MLQKQFCNKLLLDTNKENVME						LIAFDATKSAAENIVHGGLAAL
4		AATAAAATTCAGTCTGAAGGAATATGCACAAAACGAAACACACATCACGCIGAIGAIAIA	GCTAATCATGACTTTGTGTTTTTTGGCGTTGAAATCTCTAAAACATGATGATGTTTTTGATGATGTTTTTTTT	ACAAAACATCACACIGIIGAIIIIIIGGIIGCAAAIIGCGIAIAIAACAAAAAAAA	TATATGACATTAACCGATCACIIIGAIAAIGCIAIICCACCIGIIIIIGAAGAAGT	TTTTTAGATAAATTTICAGAGGIIAAIAAAAAAGAAGIIAGIIAGAATAATAATAATAATAATAATAATAATAATAATAATAA	ATAGATGTACCAATATTCAATACIAAAGAIAIGAAGIIAGGGCICGGAIAAAGTCTTGCC	ATTAGAAAAAGTGAAGACCAAAGGCIICAAGGAGIIIIIGCIAIGGAAAAAAAA	TCTGGATAGAATCATAAACTTTG1TT11 CAGCCAGAGIACCAIAIACOIAGGAT	AAAACTTCAAAAAAGTTAAGAIIAGAAAAAIAICCIIAGAGGAGGGGGGGGGG	AAGAAATTAACAAGCAGGTCACTAACAAAAAAIIGCICICCAGGCICIIIII	ATCAAAAGAGGATGTCGCCIIAIAIAIAIAIAAATTAAAAATTAAAATTCAAAATTCAAAGGTG	CATAAAGCATGAGTTG1AIGAIAIIGAGIAICIACIIAGCGCICAIGAGAAAAAAAGTAA	TGAGIAIIIIAICAAIAAGGGAATAAAATATGGGAATGCAGAAATGATAATATTATT	TECAACATCTGACAATAAATATTTAATCAAAATTGAATACGTTTAG	ATGAATATAACAACTCTGACTAATAGTATTTCCACCTCATCATTCAGTCCAAACAAT.	TCATCAACCGAAACAGTTAATTCTGATATAAAAACAACGACCAGIICICAICCIGIA	ACTATGCTCAACGACACCCTTCATAATATCAGAACAACAAAICAGGAAIIAAAAAAAAAA	ACAAAAAAGGTTGACTAAAACA GGC AGAAGAAAI AGCA I ACA I CA O CAAATAA	ATGTAAATAAATCCGCTCAACTATTGGAATATTCCAAGAAACAAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAAATCAAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAAATCAAATCAAATCAAATCAAAATCAAAATCAAAAAA	CAAGAGAATTAIIACAIICAGCCCCGAAAGAAAGAAGCGGAGOIIGATGAAAGAAGAGTATCTC	AGAGAACIGIGGGCIAAAAIIGCAAACICCAICAITTTAGCGCTGTTTTCC	GAACATGCCGTTAGTTCCCCGAGGTAACGAAACTCCGTGAAATTACAAGTCAACT	ACCOUNT CONTROL OF CON	AGGCA11GGAAGAGGAATAAATAAATAGGCTTACAGAATTAGGTGGAACAATCGGCAAGG	AAACGGGGGATATGTTGTCAGTATAAACATGACCCCAATAGACAATATGTTAAAAA	ATCTAGGTGGAAATGGCGAGGTTGTGCTAGATAATGCAAAATAICAGGCAIGGAA	CTCTGCCGAAGATGAAACAATGAAAAATAATTGAGTACAAAAATAAGGTCATGTACAA	AGIAIIIIIGAIAAIIIAGIAAAGGTGGG	ACTITIO DO A TETT CO A A TETT CO A A CO A CO A CO A CO A CO A CO A	CAAAACACAAAACCAAACCCAGACTTTATATACAGATATATCCACAAAACTCA	GAAACACAAAAATCACAAAATTATCAGCAGATTGCAGCGCATAIICCACIIAAIGI	CCCGTATTAACAACCACATTAAATGATGATGAACT AAAGT ATCAGAGATGAG	TCAGAAATCATTGCTCGCC1 ACIGACAAAAGAIGAAAAGAIGAAAAGAAAAAAAAAAAA	ACCIOCAGAGAACACIOLGGALAILI COACTAGAAACTAGAATTGGGCTCTCAATTGT	GCCGITCIACITICISCITICI SICCITICISCITICI SICCIPICI SICIPICI SICI

		AGCATTACTGGAGCAGTCACACACAGTAGGTATAACGGGTATCGGTGCCAAAAAAAA	SSSIIGAVIQVGII GIGAKKIH
		GGGALLAGUGACCAAAAAGGAGCOLLAAGAAAAAAACAAATAGATACAAATATCACCTCACCACAAACTAA	KELAGSKLGLNKQIDTNITSPQ
		CTCTAGGAGAAAATTTTTAGGTAAAAATAAACTGGCGCCAGATAATATACCCTGTCAACTGAACA	TNSSTKFLGKNKLAPDNISLST
		TAAAACTICTCITAGTICTCCCGATATTTCTTTGCAGGATAAAATTGACACCCAGAGAAGTTTA	EHKTSLSSPDISLQDKIDTQRR
		CGAGGTCAATACCCTTTCTGCGCAGCAAAACATTGGCCGTGCAACATGGAAACATCA	TYELNTLSAQQKQNIGRATME
		GCGTTGCTGGTAATATATCCACATCAGGAGGCGTTATGCATCTGCAGAAGAAGAAC	TSAVAGNISTSGGRYASALEE
		A A CTA A TO A GARDA GAR	EEQLISQASSKQAEEASQVSK
		CCAAGCGACAAATCAATTAATACAAAATTATTGAATATAATTGACAGCATCAACCAATCAAAGAA	EASOATNOLIOKLLNIIDSINOS
Shinella	9	ATGITACCGATAAATAATAACTTTTCATTGCCCAAAATTCTTTTTATAACACTATTTCCGGTACAT [1-1022] 13	_
a oHeci	,	ATECTGATTACTTTTCAGGATGGGATAAATGGGAAAAACAAGCGCTCCCCGGTGAAGAGGGTTGA	YADYFSAWDKWEKQALPGEE
5.5		Treasectrotocoacttaaagaatetcttatcaataattccgatgaacttcgactgaccgtt	RDEAVSRLKECLINNSDELRL
		TAAATCTGCTGCTACCTGACAACTTACCAGCTCAGATAACGCTGCTCAATGTATAATC	DRLNLSSLPDNLPAQITLLNVS
		A TTA A CTA COTA COTA COTA COTA COTA COT	YNQLTNLPELPVTLKKLYSASN
		CAGAATTGCCGTGCTACCTCCTGCGCTGGAGTCACTTCAGGTACAACACACAGAGCTGGAAAA	KLSELPVLPPALESLQVQHNE
		CCTGCCAGCTTTACCCGATTCGTTATTGACTATGAGTATCAGCTATAACGAAATAGTCTCCTTACC	LENLPALPDSLLTMNISYNEIV
		ATOCTOCA CAGGOTOTT AAAAA TOTOGA GOGA COGA TAATIT COTOA CIGA GOTA CAGA CAGA COGA COGA CAGA CAGA CAGA CAG	SLPSLPQALKNLRATRNFLTEL
		TTTCTCACCAAAATAATCCCGTTGTCACAGAGTATTTTTTTGATAGAAATCAGATAAGTCATATCC	PAFSEGNNPVVREYFFDRNQI
	_	COCATACCATTCTTAATCTGAGGAATGAATGTTCAATACATATTAGTGATAACCCATTATCATCCC	SHIPESILNLRNECSIHISDNPL
		A TROUTE COA A GOOG TO CAA A GOOG TO TO COA COA COA COA COA COA COA COA COA CO	SSHALQALQRLTSSPDYHGPR
		CTCCATGAGGGACAGAGAGAGATACACTCCATCGCCCCTGGCTGATGCCGTGACAGCATG	IYFSMSDGQQNTLHRPLADAV
		CTTCCCGC AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TAWFPENKQSDVSQIWHAFE
		COAACCTTTTCCGCGTTCCTTGACCGCTTTCCGATACCGTCTCTGCACGCCATACCGCCATACCTCTCGCACGCA	HEEHANTFSAFLDRLSDTVSA
		ATTCCTTO ACCOUNT OF THE CONTROL OF T	RNTSGFREQVAAWLEKLSAS
		ATTITION TOTAL TOT	AELRQQSFAVAADATESCEDR
Shinella	7	ATGAAAAATAACATTATTAAAAAACACTTTTGAGAATAATAATAATTCTCATGCTGGCA [1-612] 14	Γ
Den School	_	TAGTAACGGAGCCCATTCTCGGTAAGTTAATAGGTCGGGGGTCGACAGAAATCTTTGAAGA	VTEPILGKLIGGGSTAEIFEDV
2	_	TGTGAATGATTCATCTGCTTTGTATAAAAAGTATGATCTTATTGGCAACCAGTACAATGATTCT	NDSSALYKKYDLIGNQYNEILE
	_	GGAAATGGCTTGGCAAGAATCTGAGCTTTTTAATGCTTTTTATGGCGATGAAGCATCCGTTGTTA	MAWQESELFNAFYGDEASVVI
		TACAGTATGGCGGAGATGTGTACCTCCGAATGCTGCGCGTGCCTGGGACTCCCCTTAGTGACAT	QYGGDVYLRMLRVPGTPLSDI
		TGATACAGCTGATATCCCTGATAATATAGAGCCTTTATCTACAGTTGATATGAAATTGAAATGA	DTADIPDNIESLYLOLICKLNEL
		GTTGAGTATAATCCATTACGATCTTAATACAGGTAATATGCTGTATGATAAAGAAAG	SIIHYDLNTGNMLYDKESESLF
		ATTCCCAATAGATTTTCGCAATATTTATGCTGAATATTACGCTGCAACCAAAAAAGATAAAGAGAT	PIDERNIYAEYYAAIKKUKEIID
		TATCGACCGACGATTACAAATGCGTACAAATGATTTTTATTCGTTATTAAACAGGAAATATTTAT	HALOMRIND-YSLLNERYL'I
	_	GACGTATTTGTTGATGCTATAA	YLLIML
Tat	ple II	Table II : Bait-prey interactions	
1: Bait name	me	2: Bait nucleic 3: Prey name	

MODITAGE DILICIE

1 preyd7804 (LOC91851) https://docs.new.com/pickings/		acid SEQ ID No.	
ospet 1 projektion (LOC91851) Inhypothetical proteinXP_041083 ospet 1 projektion (LEXO3 FBX3 DKT2p6648092 FBA) hFBX03 ospet 1 projektion (LOC9187) INLANA ospet 1 projektion (LOC9187) INLANA ospet 1 projektion (LOC91873) INLANA ospet 1 projektion (LOC91873) INLANA ospet 1 projektion (LOC91870) INLANA ospet 1 projektion (LOC91870) Inhypothetical proteinXP GG3868 ospet 1 projektion (LOC91870) Inhypothetical proteinXP GG3868 ospet 1 projektion (LOC9070) Inhypothetical proteinXP GG3868 ospet 1 projektion (LOC9070) Inhypothetical proteinXP GG3868 ospet 1 projektion (LOC9070) Inhypothetical proteinXP GG3868 1 projektion (LAMBP9 HANBPM HANBP9-PENDING; proj/C01) InhANBP9 InhanBPM ospet 1 projektion (LAC907064) Inhypothetical proteinXP GG3868 1 projektion (LAC907064) Inhypothetical proteinXP GG3868 projektion (LAC9070641) InhXP GG3868 2 projektion (LAC90706765) Interfered (LAC90706765241 Inhypothetical proteinXP GG3813 projektion (LAC904106767676261 (L		-	prey44074 (JM5; prey44078) hJM5
1	Shigella ospB	-	prey67804 (LOC91851) hhypothetical proteinXP_041083
1	Shigella ospB	-	prey67806
	Shigella ospB	-	prey67810 (FBXO3 FBX3 DKFZp564B092 FBA) hFBXO3
	Shigella ospB	-	prey5237 (NONO NRB54 NMT55 P54NRB) hNONO
0sg/b 1 proe/3730 (LMO4; pre/34731) n.LMO4 0sg/b 1 proe/37314 (ZNI) ppe/37312 p.ZNI 0sg/b 1 pre/67356 (LOC1/86773) n.ZNI 0sg/b 1 pre/67357 (LOC3/6773) n.pmoptherical profemal 0sg/b 1 pre/67576 (LOC1/86774) n.pmoptherical profemAP G33663 0sg/b 1 pre/67576 (LOC3/6776) n.pmoptherical profemAP G33663 0sg/b 1 pre/67577 (LOC90706) n.pmoptherical profemAP G33663 0sg/b 1 pre/67586 (MOGA) n.pm/03A 0sg/b 2 pre/67584 1 pre/67584 pre/67589 (LOC3/6758) n.pm/03A 2 pre/67589 (LOC3/6758) n.pm/03A pre/67589 (LOC3/6758) n.pm/03A 3 2 pre/67587 (LOC3/6758) n.pm/03A pre/67581 n.pm/03A 2 pre/67589 (LOC3/6758) n.pm/03A pre/67589 (LOC3/6758) n.pm/03A pre/67589 (LOC3/6758) n.pm/03A 2 pre/67580 (LOC3/6758) n.pm/03A pre/67580 (LOC3/6758) n.pm/03A <td>Shigella ospB</td> <td>-</td> <td>prey67661 (CAPN2 CANPL2 CANPML) hCAPN2</td>	Shigella ospB	-	prey67661 (CAPN2 CANPL2 CANPML) hCAPN2
	Shigella ospB	-	prey34730 (LMO4; prey34731) hLMO4
	Shi jella ospB	-	prey33141 (ZIN; prey33142) hZIN
9898 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Shigella ospB	-	ar to 3-HYDROXYISOBUTYRATE
9056 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Shigella ospB	-	prey67608 (MGC4126) hMGC4126
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Shigella ospB	-	prey67637 (LOC90706) hhypothetical proteinXP_033663
	Shigella ospB	F	prey12713 (LMQ2 RBTNL1 RHOM2 TTG2 RBTN2; prey12714) hLMO2 hTTG-2a/RBTN-2a
	Shigella ospB	1	prey67836 (MYO9A) hMYO9A
	Shigella ospB	-	prey700 (RANBP9 RANBPM HANBP9-PENDING; prey701) hRANBP9 hRanBPM
	Shigella ospB	1	prey67844
- ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	Shigella ospB	-	prey67853
<u> </u>	Shigella ospB	-	prey66272 (FLJ20254) hFLJ20254
<u> </u>	Shigella ospD1	2	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey701) hRANBP9 hRanBPM
<u> </u>	Shigella ospD1	2	prey2492 (FLJ11026; prey2493) hFLJ11026
<u> </u>	Shigella ospD1	2	prey67651 putative homolog of prey064241 - Mouse
<u> </u>	Shigella ospD1	2	prey67653 putative homolog of prey067652 -
<u> </u>	Shigella ospD1	2	prey67667 (PACSIN2) hPACSIN2
<u> </u>	Shigella ospD1	2	prey67657 hUnknown (protein forMGC:16824)
<u> </u>	Shigella ospD1	2	prey67501 (LOC51667) hLOC51667
<u> </u>	Shingella ospD1	2	prey67678 (LOC90410) hhypothetical proteinXP_031534
<u> </u>	Shigella ospD1	2	prey67578 (LOC121052) hhypothetical proteinXP_035313
<u>a a a a a a a a</u>	Shigella ospD1	2	prey67580 (DKFZp586l021) hDKFZp586l021
<u> </u>	Shirjella ospD1	2	prey3160 (KIF5B UKHC KNS KNS1 U-KHC KINH; prey3161) hKIF5B hkinesin heavychain
2 2 2 2 2 2	Shigella ospD1	2	prey50427 (KIAA0419; prey50428) hKIAA0419
00000	Shigella ospD1	2	prey63765 (LIM; prey63767) hLIM
2 2 2 2	Shigella ospD1	2	prey67623 (LDB2 CLIM1) hLDB2
a a a	Shigella ospD1	2	prey7315 (LDB1 CLIM2 NLI; prey7316) hLDB1 hCLIM2
2 2	Shigella ospD1	2	prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1
2	Shigella ospD1	2	prey53735 (TLN1 TLN KIAA1027) hTLN1
	Shigella ospD1	2	prey67630

TOOLDEDY OLLYON

Shigella	ospD1	2	prey12665 (CREBL1 CREB-RP 013; prey12666) hCHEBL1 hG13
Shigella	ospD1	2	prey67631 (FLJ21742) hFLJ21742
Shigella	OSpD1	2	preyz0143 (SYNCOILIN; preyz0144) hSYNCOILIN
Shigella	ospD1	2	prey1418 (NR1H2 UNR NER NER-I RIP15 LXR-B; prey1419) hNR1H2 hNer-I
Shigella	OSpD1	2	prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2
Shigella	ospD1	2	prey67648 (PON2) hPON2
Shigella	ospC1	8	prey67266
Shigella ospC1	ospC1	8	prey67267
Shigella osoC1	ospC1	8	prey50590 (TID1; prey48229) hTID1
Shidella ospC1	ospC1	9	prey9822
Shidella ospC1	ospC1	8	prey67268
Shipella ospC1	ospC1	8	prey67270
Shidella	ospC1	8	prey67271 (STAT5B STAT5) hSTAT5B
hidella	ospC1	3	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey701) hRANBP9 hRanBPM
Shigella ospC1	ospC1	3	prey3486 (PM5; prey3487) hPM5 hpM5
Shigella ospC1	ospC1	8	prey14801 (KIAA0321) hKIAA0321
Shigella ospC1	ospC1	3	prey67279
Shigella ospC1	ospC1	8	prey67280
Shidella ospC1	ospC1	e	prey49194 (KIAA0211; prey49195) hKIAA0211
Shidella	ospC1	က	prey67287
Shigella	ospC1	8	prey19931 (HEF1 CAS-L) hHEF1
Shidella	ospC1	8	prey67290
Shidella	ospC1	3	prey67291
	ospC1	8	prey67294
Shidella	OSDC1	က	prey67296
	ospC1	က	prey67299
Shigella	ospC1	9	prey4637 (TAF2A BA2R CCG1 CCGS NSCL2 TAFII250; prey4638; prey4639) h1AF2A
	ospC1	ဇ	prey67316
	ospC1	က	prey67318
Shigella	ospC1	8	prey7144 (IMMT P87/89 HMP; prey7145) hIMMT hp87/89
Shinella ospC1	ospC1	m	pre/67328 (TSC22) hTSC22
Shinella osnC1	OSDC1	0	prey37430 (WASL N-WASP; prey37432) hWASL hN-WASP
Shigella ospC1	ospC1	9	prey67351
Shidella ospC1	ospC1	8	prey67353
Shigella ospC1	ospC1	3	prey25185 hHSPC272
Shigella ospC1	ospC1	3	prey4411 (ZNF147 EFP TRIM25 Z147) hZNF147
- II III-	0.00	c	AND

10043487.011202

Shigella	ospC1	20	preyo/368 (LOCSZOUS) nnypometical proteinAP_up3074
Shigella ospC1	ospC1	8	prey67371
Shigella ospC1	ospC1	က	prey4005 (KIAA0141; prey4006; prey8649; prey44107) hKIAA0141
Shigella	ospC1	8	prey67380
Shigella	ospC1	3	prey3296 (FHOS; prey3297) hFHOS
Shigella ospC1	ospC1	8	prey2108 (prey2101; prey2104; prey2107; prey2102; prey2103) hSimilar to COP9 (constitutive photomorphogenic), subunit standidonsis, homologi subunit 5 (Hisaniers)
			hCOPSS hamilton constitutive entermental Applications composite to the property of the propert
Shidella ospC1	ospC1	3	prev67403
Shigella ospC1	ospC1	3	prey67405
Shigella ospC1	ospC1	60	prey14400 (prey14399; prey14401) hprotein phosphatase 5, catalyticsubunit hPPP5C
Shigella ospC1	ospC1	3	prey50029
Shigella	ipaD	4	prey67563 (PRSC1) hPRSC1
Shigella ipaD	ipaD	4	prey2109 (COPS5 JAB1 SGN5 MOV-34; prey2110) hCOPS5 h38 kDa Mov34homolog
Shigella	peD	4	prey25185 hHSPC272
Shigella	paD	4	prey53990 (TNFRSF1A CD120a TNF-R TNF-R-I TNF-R55 TNFAR TNFR60 TNFR1 p55-R p55) hTNFRSF1A
Shigella	paD	4	prey9120 (VIM; prey9122) hVIM hvimentiin
Shigella	ipaD	4	prey6/7571
Shigella	ipaD	4	prey67572
Shigella	ipaD	4	prey65696 (KARS KIAA0070; prey65697) hKARS hLysyl tRNASynthetase
Shigella	ipaD	4	prey8889 (PLCB3) hPLCB3
Shigella	ipaD	4	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey701) hRANBP9 hRanBPM
Shigella	lpaD	4	prey2694 (INDO IDO; prey2696; prey2693) hINDO hINDO
Shigella ipaD	ipaD	4	prey53735 (TLN1 TLN KIAA1027) hTLN1
Shigella	ipaD	4	prey67574
Shigella ipaC	ipaC	22	prey67509 (POLR2A RPOL2 POLR2 POLRA hRPB220 hSRPB1 RPO2 RpilLS RPBh1 RPB1) hPOLR2A
Shigella ipaC	ipaC	2	prey67514
Shigella ipaC	ipaC	co.	prey2926 (FLJ23153; prey2927) hFLJ23153
Shigella	ipac	22	prey4458 (RRBP1 ES130 ES/130; prey4459) hRRBP1 hES/130
Shigella	ipaC	വ	prey4458 (RRBP1 ES130 ES/130; prey4459) hRRBP1 hES/130
Shigella	ipaC	വ	prey67522
Shigella ipaC	ipaC	22	prey527 (CLTC CLTCL2 KIAA0034; prey528) hCLTC hKIAA0034
Shigella	ipaC	5	prey53735 (TLN1 TLN KIAA1027) hTLN1
Shigella	ipaC	വ	prey53735 (TLN1 TLN KIAA1027) hTLN1
Shigella	ipaC	2	prey67546 (LOC128116) hsimilar to phosphodiesterase 4D interacting protein (myomegalin) (H.sapiens)
Shinella	inac	2	Drev4671 (KIAA0454) hKIAA0454

Shigella ipe	pac	ນ ໝ ໝ	preyersor (LC occord)
	pac	210	prey67473 (GALE) hGALE
1	ipaC	ro r	prey8929 (KIAAU728 FLJZ1489) IINAAU726 prey8488 (ACF7 ABP620 KIAA1251 KIAA0465) hACF7
Shinella in	pac	2 0	prey3514 (SNX1; prey3515) hSNX1
	ipaC	2	prey5814 (USP9X DFFRX) hUSP9X
	ipaC	5	prey5814 (USP9X DFFRX) hUSP9X
	ipaC	2	prey6/4/79
	ipaC	22	prey/Q0 (HAMBEM HAMBEM HAMBES FERDING, prey/ O1)
	ipaC	2	pregytati (subant about in maine (H.sapiens)
	pac	ı,	preparation in DSK2 PLIC-1 DA41 XDRP(1) hUBQLN1
	ipac	0 1	PIPS/1977 (2017) 1005 HK/AA1007
	pac	o r	programmer (28HT CSMT CSA PL; prey324; prey325) hCSH1
Chicolla in	Car	100	prev67495
1	Car	ıc	prev67506 (LOC126083) hdynamin2
	rac	2	prey4578 (PSAP SAP1 GLBA, prey5664) hPSAP hGLBA
1	pac	2	prey1135 (PSMD1 P112 S1; prey1136) hPSMD1 hproteasome subunity 112
	Dac	വ	prey67465 (COL4A2 FLJ22259) hCOL4A2
	ipac	2	prey28880 (KPNA4; prey28881) hKPNA4 hQIP
	pac	5	prey3599 (TRIP12 KIAA0045; prey3600) hTRIP12 INTANOVAS
Shigella	ipaH9.8	9	prey67717
Shigella	ipaH9.8	9	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey7.01) IIIANDF 9 IIIANDF 19 IIANDF
	ipaH9.8	9	prey67718 (KIAA1715) hKIAA1715
Shinella	inaH9.8	9	preyz530 harrestin, beta1
	ipaH9.8	9	prey67731 (LOC126896) hsimilar to Gene 33/Mig-b (H.Sablens)
	ipaH9.8	9	prey7155 (CSH2 CSB) hCSH2
	ipaH9.8	9	prey1687 (DCTN1) hDCTN1
	paH9.8	9	prey67734 (FLJ10618) hFLJ10618
	inaH9.8	9	NDO IDO; prey2696; prey2693) hINDO
	inaH9.8	9	prey67740
	ipaH9.8	9	prey67703 (PPP2R4 PTPA) hPFP2H4
Shigella	ipaH9.8	9	prey67741
Shigella	ipaH9.8	9	prey67742 (FL20313) hFL220413
	B OH cui	œ	prev67339 (MMP19 RASI-1 MMP18) nmmi-19

FOOTWARY OFFICE

Shigella ipe		ď	prev67337 (MMP19 RASI-1 MMP18) hWMP19
2000	inaH9.8	9	prey67746 (FBXO25 FBX26) hFBXO25
Shidella in	ipaH9.8	9	prey54430 (PSG4 PSG9) hPSG4
Shigella ipaH9.8	aH9.8	9	prey67749
Shigella ipaH9.8	aH9.8	9	prey67751
Shigella ipaH9.8	aH9.8	9	prey8739 (MLL2 ALR; prey8742) hMLL2 hALR
Shigella ipaH9.8	aH9.8	9	prey18232 (CCT3 TRIC5 CCTG; prey18233) hCCT3 hCctg
Shidella	ipaH9.8	9	prey66739 (EIF2B1 EIF2B EIF-2B) hEIF2B1
Shigella ipaH9.8	aH9.8	9	prey67769 (PP2135 FLJ00041) hPP2135
Shigella ipaH9.8	aH9.8	9	prey13613 (KIAA0970) hKIAA0970
Shipella	ipaH9.8	9	prey3337 (LMNA LMN1 EMD2 FPL LFP LDP1 FPLD CMD1A, prey14196) hLMNA
Shigella ip	ipaH9.8	9	prey67774 (LOC119758) hsimilar to REGULATOR OF PRESYNAPTIC ACTIVITY AEX-3 (H.sapiens)
	ipaH9.8	9	prey67776
	ipaH9.8	9	prey4758 (DKFZP761L0424 KIAA1217), hDKFZP761L0424
	ipaH9.8	9	prey67781 putative homolog of prey046760 - Mouse Fmnl
	ipaH9.8	9	prey2109 (COPS5 JAB1 SGN5 MOV-34; prey2110) hCOPS5 h38 kDa Mov34homolog
	inaH9.8	စ	prey4060 (KIAA0155; prey4061; prey4062) hKIAA0155
Shigella	ipaH9.8	9	prey49284 (SLC7A8 LAT2) hSLC7A8
Shigella ip	paH9.8	9	prey67686
	paH9.8	9	prey66872 (MRPS9) hMRPS9
	paH9.8	9	prey67690 (RRP4) hRRP4
	ipaH9.8	9	prey67695 (ATP6N1B RDRTA2 RTA1C VPP2 RTADR) hATP6N1B
	paH9.8	9	prey67336 (MMP19 RASI-1 MMP18) hMMP19
1	paH9.8	9	
	ipaH9.8	9	prey6586 (FLNA ABPX ABP-280 FLN FLN1 NHBP; prey6587) hFLNA
	ipaH9.8	9	prey56789 (ALDH4 P5CDH; prey56791) hALDH4 hP5CDh
	ipaH9.8	9	prey67711
	ipaH9.8	9	prey2118 (RNF2 dinG Bap-1; prey2119) hRNF2 hring finger proteinBAP-1
	ipaH9.8	9	
Shigella ip	іраН9.8	9	prey666 (RANBP16 KIAA0745; prey667; prey665; prey9721) hHANBP16 hHAN binding proteinto infanbP16 hRANBP16
Shigella ospG	spG	7	prey3917 (BTBD2 FLJ20386; prey3920; prey3918; prey3921; prey3922; prey3919) hBTBD2
Shigella ospG	spG	7	prey63632 (ZNF189; prey63789) hZNF189
Shigella ospG	spG	7	preyz109 (COPS5 JAB1 SGN5 MOV-34; preyZ110) hCOPS5 h38 kDa Mov34homolog
Shigella ospG	spG	7	prey54201 (UBE2D3 UBCH5C; prey54202), hUBE2D3 hUBCH5C
Shigella ospG	spG	7	prey1922 (DLST DLTS; prey1923) hDLS hEZK
Shigella ospG	SpG	7	prey67418 (UBE2L3 UBCH7) hUBE2L3

IOD+SHEZ OLILOE

Shipella osp. 7 7 7 7 7 7 7 7 7	
Singella 0590 7 7 7 7 7 7 7 7 7	prev67435 hUnknown (protein forMGC:3432)
Shippella osyconomics 7 7 7 7 7 7 7 7 7	prev(67443 (FLJ11807) hFLJ11807
Shipplia 0st/C 7 7 7 7 7 7 7 7 7	prev67317 (KIAA1485) hKIAA1485
Singella ostock 7 7 7 7 7 7 7 7 7	prev67393 (UBE2D2 UBCH5B UBC4) hUBE2D2
Shigella ostod 7 7 7 7 7 7 7 7 7	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey701) hRANBP9 hRanBPM
Shigella osp.G 7 Shigella osp.G 7	prey67411 (UBE2E3 UBCH9) hUBE2E3
Shigella ospG 7 Shigella ospG 7 Shigella ospG 7 Shigella ospG 7 Shidella ospG 7	prey67423
Shigella ost G 7	prey67298
Shigella ospG 7 Shigella ospG 7 Shigella ospG 7	prey67464
Shigella osrG 7 Shigella osrG 7	prey67320
Shiqella ospG 7	prey67321
	prey35777 (PSG2 PSBG2 PSGGB; prey35778) hPSG2 hPSG1
Shipella penG	prev67327 (AKAP13 HT31 BRX) hAKAP13
Shinella osnG	prey412 (RPN2; prey413) hRPN2 hsignalpeptide
Shinella osoG	prey50598 (PEX10 NALD; prey50599) hPEX10 hperoxisome assembly proteinPEX10
Shioella ospG 7	prey67364
Shinella ospG	prey67367
Shipella osnG	prey67369
Shigella osug	prey67372 (CD63 MLA1 ME491) hCD63
Shipella ospG 7	prey67379
Shigella ospG 7	prey67381 (LOC131541) hhypothetical proteinXP_059524

HOUTHER, LOFFICH

	Coo other comments and contract
1 gblAB008515 AB008515 Homo sapiens mKNA for HanBPM, complete cds.	lanbrw, complete cus.
1 gb AC005091 AC005091 Homo sapiens BAC clone CTA-318C11 from 7p14-p15, complete sequence.	CTA-318C11 from 7p14-p15, complete sequence.
1 gb AF117888 AF117888 Homo sapiens myosin-IXa mRNA, complete cds.	mRNA, complete cds.
1 gb/AF141347/AF141347 Homo sapiens hum-a-tub2 alpha-tubulin mRNA, complete cds.	alpha-tubulin mRNA, complete cds.
1 gb AF176702 AF176702 Homo sapiens F-box protein FBX3 mRNA, partial cds.	n FBX3 mRNA, partial cds.
1 gb/AF177198/AF177198 Homo sapiens talin mRNA, complete cds.	complete cds.
1 gb AF212940 AF212940 Homo sapiens zinedin (ZIN) mRNA, complete cds.) mRNA, complete cds.
1 gb/AF257211/AF257211 Homo sapiens LMO2b splice variant (LMO2) mRNA, complete cds.	se variant (LMO2) mRNA, complete cds.
1 gb/AJ005897/HSA005897 Homo sapiens mRNA fi Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).	gb/AJ005897HSA005897 Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53537, LLNLC110F1057 Q7 (n.g.f. Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).
1 gb/aK024239/aK024239 Homo sapiens cDNA FLJ14177 fis, clone NT2RP2003161	4177 fis, clone NT2RP2003161.
1 gb AL049176 HS141H5 Human DNA sequence fro protein with von Willebrand factor type C domain	gb/AL049176/HS141H5 Human DNA sequence from clone 141H5 on chromosome Xq22.1*23. Contains parts of a mover chromin chromosome yeples sequence. Protein with von Willebrand factor type C domains. Contains ESTs, STSs and GSSs, complete sequence.
1 gb AL122043 HSM801240 Homo sapiens mRNA;	gb AL122043 HSM801240 Homo sapiens mRNA; cDNA DKF22566G1424 (from clone UKr-25b660 4444).
1 gb AL42166 HSMX1A Homo sapiens chromosor complete sequence.	gp AL4g166 HSMX1A Homo sapiens chromosome 21 from 5 PACs and 5 Cosmids map 21qzz.z,Uz15s49-wA1, segmen 7z, complete sequence.
1 ablAP002026 AP002026 Homo sapiens genomic	oblAP002026IAP002026 Homo sapiens genomic DNA, chromosome 4q22-q24, done:429K21, complete sequence.
1 gb D21260 HUMORFEA Human mRNA for KIAA0034 gene, complete cds.	34 gene, complete cds.
1 gb L14599 HUMPSFHOMO Human mRNA, complete cds.	te cds.
1 gblL28809 HUMAAE Homo sapiens dbpB-like protein mRNA, complete cds.	in mRNA, complete cds.
1 gb M23254 HUMCANP Human Ca2-activated neu	gb M23254 HUMCANP Human Ca2-activated neutral protease large subunit (CANP) mHNA, complete cds.
1 gb U24576 U24576 Homo sapiens breast tumor autoantigen (LMO4) mRNA, complete cds.	oantigen (LMO4) mRNA, complete cds.
1 gb X61118 HSTTG2 Human TTG-2 mRNA for a cysteine rich protein with LIM motti.	steine rich protein with LIM motif.
2 gb/AB007879/AB007879 Homo sapiens KIAA0419 mRNA, complete cds.	mRNA, complete cds.
2 gb/AB008515/AB008515 Homo sapiens mRNA for RanBPM, complete cds.	RanBPM, complete cds.
2 gb AB016485 AB016485 Homo sapiens mRNA fo	gb/AB016485/AB016485 Home sapiens mRNA for LIM homeobox protein cofactor (CLIM-2), complete cds.
2 gb AB028956 AB028956 Homo sapiens mRNA for KIAA1033 protein, partial cds.	KIAA1033 protein, partial cds.
	KIAA1288 protein, partial cds.
	gb AC003108 HUAC003108 Human Chromosome 16 BAC clone CIT 8875X-32 / Oz4, complete sequence.
2 gb/AC008764/AC008764 Homo sapiens chromosome 19 clone C I D-3Z2Z2D1 9, complete sequence.	ne 19 clone CTD-3ZZZD19, complete sequence.
2 gb/AF001601/AF001601 Homo sapiens paraoxonase (PON2) mHNA, complete cds.	se (PONZ) mRNA, complete cas.
	specific formin related protein (FTI) mistry, complete cus.
	I mHNA, complete cas.
	specific formin related protein (Fr1 mRNA, complete cds.

ADDUSTED DILIDE

		1111 Oli 1111 DAIL A CONTRACTOR AND
ospD1	2	gb AF068651 AF068651 Homo sapiens LIM-domain binding factor or the Computer Compute
ospD1	7	gb/AF128536/AF128536 Homo sapiens cytoplasmic phosphoprotein PACSINZ mHNA, complete cus.
ospD1	2	gb AF155099 AF155099 Homo sapiens NY-REN-18 antigen mHNA, complete cds.
ospD1	2	gb AF177198 AF177198 Homo sapiens talin mRNA, complete cds.
ospD1	2	gblAF265342 AF265342 Homo sapiens chromosome 8 map 8p BAC 2053/021, complete sequence.
ospD1	7	gb/AK001888/AK001888 Homo sapiens cDNA FLU1026 fis, clone FLACE1004104.
ospD1	2	gb/AL121808 CNS01DSJ Human chromosome 14 DNA sequence *** IN PROCHESS *** BAC C-2313O13 or initially carred to include the control of the con
1000	c	ALA CONSORIA TO PROPERTY BPC-11-469115, T.J. RPCI-11 Homo sapiens genomic clone RPCI-11-469115 , DNA sequence.
ospD1	40	gun auch or production of the Common September 2003 of the Common September 2003 of the Sequence.
ospD1	2	gplM57298 HUMGPG25K Human GTP-binding protein G25K mRNA, complete cds.
ospD1	2	gb M63960 HUMPRPHOS1 Human protein phosphatase-1 catalytic subunit mRNA, complete cds.
ospD1	2	gb U07132 HSU07132 Human steroid hormone receptor Ner-I mRNM, complete cds.
ospD1	2	gb[U31903]HSU31903 Human CREB-RP (creb-rp) mRNA, complete cds.
ospD1	2	gb[U37519]HSU37519 Human aldehyde dehydrogenase (ALDH8) mRNA, complete cds.
ospD1	2	gb X65873 HSKHCMR H.saplens mRNA for kinesin (heavy chain).
ospD1	2	gb X65873 HSKHCMR H.sapiens mRNA for kinesin (heavy chain).
ospD1	2	gb X65873 HSKHCMR H.sapiens mRNA for kinesin (heavy chain).
ipaD	4	gb AB008515 AB008515 Homo sapiens mRNA for RanBPM, complete cds.
Dadi	4	gb[AF161390 AF161390 Homo sapiens HSPC272 mRNA, partial cds.
Dad	4	gb AF177198 AF177198 Homo sapiens talin mRNA, complete cds.
ipaD	4	gb D32053 D32053 Homo sapiens mRNA for Lysyl tRNA Synthetase, complete cds.
Dadi	4	gb D55696 D55696 Homo sapiens mRNA for cysteine protease, complete cds.
Dadi	4	gb M1414HUMVIM Human vimentin gene, complete cds.
Dadi	4	gb M34455 HUMIGIIDO Human interferon-gamma-inducible indoleamine 2,3-dioxygenase (IUO) mHNA, complete cus.
Dadi	4	gb M63121 HUMTNFRC Human tumor necrosis factor receptor (TNF receptor) mHNA, complete cds.
Dadi	4	gb U70734 HSU70734 Homo sapiens 38 kDa Mov34 homolog mRNA, complete cds.
Dadi	4	qp Z26649 HSPPLCB3 H.sapiens mRNA for phospholipase C-b3.
Dadi	4	gb Z26649 HSPPLCB3 H.sapiens mRNA for phospholipase C-b3.
ipaC	2	gb AB002366 AB002366 Human mRNA for KIAA0368 gene, partial cds.
ipaC	22	gb AB002533 AB002533 Homo sapiens mRNA for Olp1, complete cds.
ipaC	2	gb AB007923 AB007923 Homo sapiens mRNA for KIAA0454 protein, partial cds.
ipaC	22	gb/AB008515/AB008515 Homo sapiens mRNA for HanBFM, complete cds.
pac	2	gb AB018271 AB018271 Homo sapiens mRNA for KIAA0728 protein, partial cds.

Ced	r.	lablAB020335IAB020335 Homo sapiens Pancreas-specific TSA305 mRNA , complete cds.
Cad	, co	objAB023224JAB023224 Homo sapiens mRNA for KIAA1007 protein, partial cds.
Cac	rc	obj 8029290/AB029290 Homo sapiens mRNA for actin binding protein ABP620, complete cds.
pac	co Co	jah 8046026 AB046026 Macaca fascicularis brain cDNA, clone: OccE-16688.
pac	S	gb AC003991 AC003991 Human BAC clone CTB-167B5 from 7q21, complete sequence.
pac	2	gb AC005578 AC005578 Homo sapiens chromosome 19, cosmid F20887, complete sequence.
pac	2	gb/AF006751/AF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	2	gbJAF006751 JAF006751 Homo sapiens ES/130 mRNA, complete cds.
ipac	2	gbJAF006751/AF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	5	gblAF006751IAF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	2	gbjAF100153JAF100153 Homo sapiens connector enhancer of KSR-like protein CNK1 mHNA, complete cas.
ipaC	2	gbjAF176069JAF176069 Homo sapiens ubiquilin mRNA, complete cds.
pac	2	gbJAF176069JAF176069 Homo sapiens ubiquilin mRNA, complete cds.
ipaC	2	gb/AF176796/AF176796 Homo sapiens putative glialblastoma cell differentiation-related protein (GBDM) minior compened cus.
ipac	2	gblAF176796/AF176796 Homo sapiens putative glialblastoma cell differentiation-related protein (ubbry, complete cus.
Cedi	ı,	db/AF176796/AF176796 Homo sapiens putative glialblastoma cell differentiation-related protein (GBUH1) mHNA, complete cds.
Daci	C)	db/AF177198/AF177198 Homo sapiens talin mRNA, complete cds.
Cedi	ľ	cbjAF177198/AF177198 Homo sapiens talin mRNA, complete cds.
Cedi	ıc	chhAF187859 AF187859 Homo sapiens Hsp70 binding protein HspBP2 mRNA, complete cds.
Dad	LC LC	abjAF189009JAF189009 Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.
Cedi	LC LC	dbjAK000982/AK000982 Homo sapiens cDNA FLJ10120 fis, clone HEMBA1002863.
Cedi	ıc	abiD21260IHUMORFEA Human mRNA for KIAA0034 gene, complete cds.
inac.	, c	nphp28476HUMKG1C Human mRNA for KIAA0045 gene, complete cds.
i car	ıc	chip 124466 Dano sapiens mRNA for proteasome subunit p112, complete cds.
Ced	2	abl/000118IHUMPLB Human placental lactogen hormone (PL-4) mRNA, complete cds.
inac	2	gbl.00118IHUMPLB Human placental lactogen hormone (PL-4) mRNA, complete cds.
ipaC	5	gbl004164 HUM927A Human interferon-inducible protein 9-27 mRNA, complete cds.
ipaC	5	gbl[136983]HUMDNM Homo sapiens dynamin (DNM) mRNA, complete cds.
ipaC	2	gol[41498]HUMPTI1B Homo sapiens longation factor 1-alpha 1 (PTI-1) mRIA, complete cds.
ipaC	2	gb[L41668]HUMGALE Homo sapiens UDP-galactose-4-epirnerase (GALE) mRNA, complete cds.
ipaC	ις	gb M24766 HUMCOL4A2P Human (clone pHAIV2-12) alpha-2 collagen type IV (CUL4A2) mHNA, 3 end.
ipaC	ည	gbjM81355JHUMSPHINO Homo sapiens sphingolipid activator proteins 1 and 2 processed mutant minky, complete cus-
ipaC	ည	gbl/002389 HSU02389 Human hLON ATP-dependent protease mHNA, nuclear gene encoding innoctional protein, compace was
ipaC	S.	gblU53225 HSU53225 Human sorting nexin 1 (SNX1) mRNA, complete cds.

TOTALO, ZBHEHOOT

		1 Processing and 11
ipaC	2	gb/X05610/HSC4AZ Human mHNA for type IV colladerl alpira (z) crain.
ipaC	2	gb X63564 HSRPIILS H.sapiens mRNA for RNA polymerase II largest subunit.
ipaC	ည	gb/X98296 HSUBIQHYD H.sapiens mRNA for ubiquitin hydrolase.
ipaC	သ	gb Z26649 HSPPLCB3 H.sapiens mRNA for phospholipase C-b3.
ipaH9.8	9	dbj AB001636.1 AB001636 Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds
ipaH9.8	9	dbj/AB002333.1/AB002333 Human mRNA for KIAA0335 gene, complete cds
ipaH9.8	9	dbj/AB008515.1/AB008515 Homo sapiens mRNA for RanBPM, complete cds
ipaH9.8	9	dbj AB023187.1 AB023187 Homo sapiens mRNA for KIAA0970 protein, complete cds
ipaH9.8	9	dbj/AB033043.1 AB033043 Homo sapiens mRNA for KIAA1217 protein, partial cds
ipaH9.8	9	dojjaK001451.1JAK001451 Homo sapiens cDNA FLJ10589 fis, clone NT2RP2004389, weakly similar to PHOBABLE WII OCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR
ipaH9.8	9	dbj AK024449.1 AK024449 Homo sapiens mRNA for FLJ00041 protein, partial cds
ipaH9.8	9	dbj D63875.1 D63875 Human mRNA for KIAA0155 gene, complete cds
ipaH9.8	9	emb AL034405.16 HS537K23 Human DNA sequence from clone HP4-537K23 on chromosome Xq25-20.1, complete sequence
		[Homo sapiens]
B.6Hadi	9	emb AL03447.14 HS215D11 Human DNA sequence from clone 215D11 on chromosome 1056.12-33.3 Confidents a gene for a niver-
		binding protein regulatory subunit, a gene similar to rat gene 33, a pseudogene similar to FLA-A, ESI 5, SI 55, GSSS and SPG
		islands, complete sequence [Homo saple
ipaH9.8	9	emb/AL 050313.6/HSBK754D9 Human DNA sequence from clone CTA-754D9 on chromosome 22 Contains GSSs, complete sequence Homo capiens
0 0 0	ď	proving 11748 1HSMR00958 Homo sapiens mRNA: cDNA DKFZp586B1417 (from clone DKFZp586B1417); partial cds
1001		with the second state of the second s
ipaH9.8	9	emb AL13/Ubb. 1U AL13/Ubb ruinlair Divas sequence non concern and
ipaH9.8	9	emb X53416.1 HSABP280 Human mRNA for actin-binding protein (filamin) (ABP-280)
ipaH9.8	9	emb X73478.1 HSPTPAA H.sapiens hPTPA mRNA
ipaH9.8	9	emb X74801.1 HSHUMAPC H.sapiens Cctg mRNA for chaperonin
ipaH9.8	9	emb X95648.1 HSEIF2BAS H.sapiens mRNA for eIF-2B alpha subunit
ipaH9.8	9	gb/AC005392.1/AC005392 Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence
ipaH9.8	9	gb/AC005833.1/AC005833 Homo sapiens 12p13.3 BAC RPC11-234B24 (Roswell Park Cancer Institute Human BAC Library)
		complete sequence
ipaH9.8	9	gb AC005881.3 AC005881 citb_79_e_16, complete sequence [Homo sapiens]
ipaH9.8	9	gb/AC020663.1/AC020663 Homo saplens chromosome 16 clone RPCI-11_12/120, complete sequence
ipaH9.8	9	gb/AF006466.1/AF006466 Mus musculus lymphocyte specific formin related protein (Fr1) mHNA, complete cus
ipaH9.8	9	gb AF010404.1 AF010404 Homo sapiens ALR mHNA, complete cds

MUTHIC AMERICA

ipaH9.8	9	gb AF064729.1 AF064729 Homo sapiens RAN binding protein 16 mHNA, complete cds
ipaH9.8	9	gb AF084940.1 AF084940 Homo sapiens beta-arrestin 1B mRNA, complete cds
ipaH9.8	9	gb AF135159.1 AF135159 Homo sapiens GMP reductase mRNA, complete cds
ipaH9.8	9	gb AF139184.1 AF139184 Homo sapiens Sec31 protein mRNA, complete cds
ipaH9.8	9	gb AF141327.1 AF141327 Homo sapiens ring finger protein BAP-1 mRNA, complete cds
ipaH9.8	9	gb AF171669.1 AF171669 Homo sapiens glycoprotein-associated amino acid transporter LAT2 (LAT2) mRNA, complete cds
ipaH9.8	9	gb AF174605.1 AF174605 Homo sapiens F-box protein Fbx25 (FBX25) mRNA, partial cds
ipaH9.8	9	gb AF207661.1 AF207661 Homo sapiens sodium bicarbonate cotransporter-like protein mRNA, partial cds
ipaH9.8	9	gbIAF245517.1 [AF245517 Homo sapiens vacuolar proton pump 116 kDa accessory subunit (ATPBN1B) mHNA, complete cds, alternatively spliced
ipaH9.8	9	gbjAF249874.1jAF249874 Homo sapiens vacuolar proton pump 116 kDa accessory subunit gene, exon 3 and 5' untranslated region, parial sequence
ipaH9.8	9	gb J00118.1 HUMPLB Human placental lactogen hormone (PL-4) mRNA, complete cds
ipaH9.8	9	gb L14283.1 HUMPROKINC Human protein kinase C zeta mRNA, complete cds
ipaH9.8	9	gb L25286.1 HUMCOLXVA1 Homo sapiens alpha-1 type XV collagen mRNA, complete cds
ipaH9.8	9	gb M13451.1 HUMLAMC Human lamin C mRNA, complete cds
ipaH9.8	9	gb M21616.1 HUMPDGFR Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds
ipaH9.8	9	gb M32053.1 HUMH19 Human H19 RNA gene, complete cds
ipaH9.8	9	gb M34455.1 HUMIGIIDO Human interferon-gamma-inducible indoleamine 2,3-dioxygenase (IDO) mRNA, complete cds
ipaH9.8	9	gb M94890.1 HUMPSBG11 Human pregnancy-specific beta-1-glycoprotein 11 (PSG11) mRNA, complete cds
ipaH9.8	9	gb M98478.1 HUMTGH1A Human transglutaminase mRNA, complete cds
ipaH9.8	9	gb U24267.1 HSU24267 Human pyrroline-5-carboxylate dehydrogenase (P5CDh) mRNA, short form, complete cds
ipaH9.8	9	gb U37791.1 HSU37791 Homo sapiens clone rasi-1 matrix metalloproteinase RASI-1 mRNA, complete cds
ipaH9.8	9	gb U38431.1 HSU38431 Human clone rasi 6 matrix metalloproteinase RASI-1 mRNA, splice variant, complete cds
ipaH9.8	9	gb U65928.1 HSU65928 Human Jun activation domain binding protein mRNA, complete cds
ipaH9.8	9	ref[NM_014285.1] Homo sapiens homolog of Yeast RRP4 (ribosomal RNA processing 4), 3-5'-exoribonuclease (HHP4), mHNA
ipaH9.8	9	ref[NM_017762.1] Homo sapiens hypothetical protein FLJ20313 (FLJ20313), mRNA
ipaH9.8	9	ref[NM_018155.1] Homo sapiens hypothetical protein FLJ10618 (FLJ10618), mRNA
osbG	7	gb AB008515 AB008515 Homo sapiens mRNA for RanBPM, complete cds.
Spgso	7	gb AB013818 AB013818 Homo sapiens PEX10 mRNA for peroxisome biogenesis factor (peroxin) 10, complete cds.
osbG	7	gb AB033054 AB033054 Homo sapiens mRNA for KIAA1228 protein, partial cds.
osbG	7	gb AB033054 AB033054 Homo sapiens mRNA for KIAA1228 protein, partial cds.
osbG	7	gb AB040918 AB040918 Homo sapiens mRNA for KIAA1485 protein, partial cds.
osbG	7	gb/AC005281/AC005281 Homo sapiens PAC clone RP4-722F20 from 7q31.1-q31.3, complete sequence.

IDD FEFFEY DILLION

		egulations at a contract of the property of the second of
Spgso	7	gb AE003603 AE003603 Drosophila melanogaster genomic scarrior 1420000 I posocota section 1970 Company of the property of the p
osbG	7	gb AF033095 AF033095 Homo sapiens testis enhanced gene transcript protein (TECLT) IntrivA, complete cus.
osbG	7	gb AF035121 AF035121 Homo sapiens KDR/flk-1 protein mRNA, complete cds.
ospG	7	gb AF061736 AF061736 Homo sapiens ubiquitin-conjugating enzyme Htd-B mHnA, complete cos.
osbG	7	gb AF085362 AF085362 Homo saplens UbcM2 mHNA, complete cos:
ospG	7	gb[AF104913]AF104913 Homo sapiens eukaryotic protein synthesis initiation ractor invex, comprete consistence (SIAT4A)
osbG	7	gb AF155238 AF155238 Homo sapiens BAC 180k23 chromosome 8 map 644.3 belar-galacusatus alpha 2,5 sayiman sayiman
		gene, complete sequence.
ospG	7	gb AJ000519 HSUBICONJ Homo sapiens mRNA for ubiquitin-conjugating enzyme UbcH7.
osbG	7	gb AK000393 AK000393 Homo sapiens cDNA FLJ20386 fils, clone KAIA184.
ospG	7	gb AK001311 AK001311 Homo sapiens cDNA FLJ10449 fis, clone N1 ZHP1000941, nightly strilled to numer Lz uorquent
		enzyme UbcH58 mRNA.
ospG	7	gb AL050321 HSJ717M23 Human DNA sequence from clone HP4-717M23 on circumscribe zu, comprete sequence:

INDVERSE DILICE

Table	Table III: SID®					October 2 Old and a construction of the constr
1: Bait name	2: Bait nucleic acid SEQ ID No.	3. Prey name	SID nucl eic acid		amino- acid ID No.	r. SID allilloravid sequence
Shigella ospB	-	prey44074	5 5	00 €	216	FSHOSSP(CASSOKGTVH) FALKDTRINRFSALARVGK VGPMIGOYVDSOW SLASF VSPMIGOYDCAFGRITTSKN NVSVIAICONGTHKYNTTP DGNCNREAFDVYLDICDDD DF*
Shigella ospB	-	prey67804	16	GACCAGCAGTOTTGCGAGTALACATTGGGCAACTTACCAAGTGGAGAGGT GTCGTAGCTGAGGGGTCTTTCAGAATCGGCAACCAATCAAT	7.5	INSAGEMENT INCURED IN SANGER IN A REGIEONHOPHOCTOCOS SEGNIVOCTIONS SEGNIVOCTOCOS SEGNIVOCTOCOS OCASTIVOPHORIBA HAFMARINDEPSINADA OLOS SEGNIVOLINININICHAND OLOS SEGNIVOLINININICHAND OLOS SEGNIVOLINININININININININININININININININININ
Shigella ospB	-	prey67806	17	NCTNOCCTGNGCGNGACCAGCCTGGTNANCTTACCNGGANCCACNGGATGT 218 NGTGTANCTGTGCTCTGCGCTTGCCATGATGACTNTGGGAGCTGCANCOG TCGCGTTTNTGNNNCGTNGTTGGTGNCNGGCCTCCNTANGNIGTGNNACGA	218	XXLXXTSLVXLPGXTGCXV XVLCACHDDXWELXPSRX XXVVGXXPPXXVXRRLXFA

INDERHAY DIESE

				VIVO BOLLONG TOTAL
			AGACTGTTNITTGCTAAGGACCTGCNGTNTGCTGCTTCATTNGGNGAGNITT NNTTAGGGGGGGNTTATTNTTATNCTAAAATNTTGGGACTCTTAAGTTTNGNTGN OOGGAGGGGGGNAAAAAAAAAAAAAAAAAAAAAAAAA	KDLXXAASXGEXXLGGALA LKXWDS*VXXXVFXXK
			GGIIIIINNAAAAA	AAMETETAPLTLESLPTDPL
Shigella 1	prey67810	8	GGGGGCCA GGAGACCGAGGCGCGCGCGCGCGCGCGCGC	LLILSFLDYRDLINCCYVSR
gdso			TETTETTATETCAGTCGAAGACTTAGCCAGCTATCAAGTCATGATCCGCTGT	RLSQLSSHDPLWHRHCKK
			GGAGAGACATTGCAAAAAATACTGGCTGATATCTGAGGAAGAGACACA	YWLISEEEKTOKNOCWKSL
			GAAGAATCAGTGTTGGAAATCTCTTCATAGATACTTACTCTGATGTAGGAA	HDI YSDVGRYIDH YAAIKN
			GATACATTGACCATTATGCTGCTATTAAAAAGGCCTGGGATGATCTCAAGAAA	AWDDLKK TEPROFINIVE
			TATTTGGAGCCCAGGTGTCCTCGGATGGTTTTATCTCTGAAAGAGGGIGCIC	SENEGARDEDEDAVEAGE
			GAGAGGAAGACCTCGATGCTGTGGAAGCGCAGATTGGCTGCAAGCITCCIG	VARBELL COMAL SNHYBSED
		_	ACGATTATCGATGTTCATACCGAATTCACAATGGACAGAAGTTAGTGGTTCCT	VVPGELGSIMALSIVA INSEE
	_		GGGTTATTGGGAAGCATGGCACTGTCTAATCACTATCGTTCIGAAGAIIIGII	VCI DI TECHTICI SOVIAVE
			AGACGTCGATACAGCTGCCGGAGGATTCCAGCAGAGACAGGGACIGAAAIA	AAEGBNIKNEVEYOCPDOM
			CTGTCTCCCTTTAACTTTTTGCATACATACTGGTTTGAGICAGIACAIAGCAG	ADNOVATIONALIGATETDIWE
			TGGAAGCTGCAGAGGCCGAAACAAAATGAAGTTTTCTACCAAIGICCAGA	TOWNS OF THE PROPERTY OF THE P
			CCAAATGGCTCGAAATCCAGCTGCTATTGACATGTTTATTATAGGTGCLACII	ISTANIA SECTION AND A SECTION
	_		TTACTGACTGGTTTACCTCTTATGTCAAAAATGTTGTATCAGGTGGCTTCCCC	STORING SOVIED ASS
		_	ATCATCAGAGACCAAATTTTCAGATATGTTCACGATCCAGAATGTGTAGCAAC	SI SPLYELSSVAPPRITIFI I
		_	AACTGGGGATATTACTGTGTCAGTTTCCACATCGTTTCTGCCAGAACTTAGC	RIKIEMSKUALTEKACALUS
			CTGTACATCCACCCCACTATTTCTTCACATACCGAATCAGGATTGAAATGTCA	HYWHII NAKGUVEEVGGF
			AAAGATGCACTTCCTGAGAAGGCCTGTCAGTTGGACAGTCGC AI GGAGAA	THE TOTAL OF THE TOTAL
			TAACAAATGCTAAGGGTGACGTGGAAGAAGTTCAAGGACCTGGAGTAGIIG	VICTORIAL INTEGRAL IN
_			GTGAATTTCCAATCATCAGCCCAGGTCGGGTATATGAATACACAAGCIGIAC	י יייייייייייייייייייייייייייייייייייי
			CACATTCTCTACAACATCAGGATACATGGAAGGATATTATACCTTCCATTITC	FRVSIAHLVS
			TTTACTTTAAAGACAAGATCTTTAATGTTGCCATTCCCCGATTCCATATGGCAT	
			GTCCAACATTCAGGGTGTCTATAGCCCGATTGGTAAGTTAA	ACCONVENENTIA
Shinella	prev5237	19	GCAGCAACAGCAGCAGCGCCACCACCGCCAATACCTGCAAATGGGCAACA	COONEGI TIDI KNEBKPGE
osnB Buso			GGCCAGCAGCCAAAATGAAGGCTTGACTATTGACCIGAAGAAIIIIAGAAAAA	KTETOBSBI EVGNI PPDITE
1			CCAGGAGAGAGCCTTCACCCAACGAAGCCGICIIIIIGIGGGAAAIUII	CEMBRI FEKYGKAGEVEIH
			CTCCCGACATCACTGAGGAAGAATGAGGAAACIAIIIGAAAAIAIGAGAAA	KOKGEGEIBI ETBTI AFIAK
	_		GGCAGGCGAAGTCTTCATTCATAAGGATAAAGGATTTGGCIIIAICCGCIIG	VELDNMPI BGKOLBVRFA
		_	GAAACCCGAACCCTAGCGGAGATTGCCAAAGIGGAGCIGGACAAIAIGCCA	CHSASI TVBNI POYVSNEL
		_	CTCCGTGGAAAGCAGCTGCGTGTGCGCTTTGCCTGCCAIAGIGCAICCTTA	I FEA ESVEGOVEBAVVIVD
		_	CAGTTCGAAACCTTCCTCAGTATGTGTCCAACGAACTGCTGGTGAAGAAGAGGA	DRGRPSGKGIVEFSGKPAA
			TTCTGTGTTTGGCCAGGTAGAGAGGCTGTAGTGTGTGTGT	RKAI DRCSFGSFLLTTFPR
			AGGCCCTCAGGAAAAGGCATTGTTGAGTICICAGGGAAAGCCAGCIGCICAG	PVTVFPMDOLDDFEGLPEK
			AAAGCTCTGGACAGACAGGCICCIICCIGCIAACAGAGAGACTTC	LVIKNOOFHKEREOPPRFA
		-	GTCCTGTGACTGTGGAGCCCATGGACCAGTTAGATGATGATGATGATGATGATGATGATGATGATGA	

IOOTSTOY DILLION

			CAGAGAAGCTGGTTATAAAAACCAGCAATTTCACAAGGAACGAGAGCGCCCACCAGATTTCCACAAGTTGCATGCGTGGAATTTGCACAAGCCTGGTTCCTTTGAGTATGAATATGCCATGCGCTGGAAGCAGCAGCAGGACCAAGTGGACCGAACAAGCAGCAGGACCAAGTGGACCGAACAAGAAGAAGCAAGC	QPGSFEYEYAMRWKALIE MEKQQQDQVDRNIKE
Shigella ospB	prey67661	20		GDPCINTSEKKADVQAVO DEIEANLEEDISEDDIDOO VRRIEAQLAGEDAEBAEL GTILRHVAKRODINSDGS ETVERWAMADSDGSGSK GKEPYLWYKQKYGKYR GLKEPYLWYKQKYGKYR GLKEPYLWYKQKYGKYR GLKEPYLWYKQKYGKYR GLKEPYLWYKQKYGKYR EAGARWPCQLHOVIVNAR ADDQLIIDFDNYPACLVALE INKIRCQLIPENTGTIELDL ISWLCFSVL*
Shigella ospB	prey34730	21	TITIGETGATICGGGGAGAGGGTTGGAGGGCGCCCCCCGGGTAGGGGCGGCTC CCTCTCTCTGGAAGCGGTGCGCAGGGTGCGGAATGCCGGCTC TTCTGCTTGAAGCGGTGCGCAGGCTGCGGGGGCAAGATTGCGGAATGCCT TTCTGCTTGAAGCGTTGCGACAGCTTGGCACAGCCGTTGTAACCCAAAG TGGCAGCGCTTTGCACAATGCTACATTAGGTTATTTGGAAATAGCGAAG TGGCAGCCGTTTGCGACAATGCATTACATTA	MNNPGSSOPPPYTAGSI. SWKRCAGCGGKADPFLIY AMDSYWHSPCLKCSCCOA CLGDIGSTYKSSBMICR NDYHLFGNSGAGCGGCAGCGGC ITASELWARAGGNYHKC FTCSTCRNRL VPGDRFHYI NGSLFCEHDRFTALINGHL NSLGSNP
Shigella ospB	prey33141	22	CCTGAGOTIGCGGGGGATCCTGGACTTTATCCAGGCAGGTIGGGGGGGGTT 223 CGAAGCCGAGAAAGCGCGAGCGGAGCGGAGTIGGGGGGGTTACAGGGT AGGTGGGGGGAGAAAGGGCAGGAGAAAACTTAAAAGGGCAGGAAAATTTAAAAGGGCAGGAAAAGGG ACCTGGTTGCGGCGATCTAAAGTGGTAAGATTTAGAAAAGGG CCAAATTTACATAAACTGAABTTTGGGAAAGAGCTGAACCAGGGGAAAAGGG AGCAAATTTACATAAACTGAABTTTGGGAAAGAGCTGAACCAGGGGGAAAAGGG AGCAAATTGATAAACTGAABTTTGGGAAAGACCTGAACCAGGGGGAAAAGGG GGAAAAACAGCCGTTGGTGGAACAATGGCCCGGTGGAATTCGGTCACCCT AGGAAAAAAACAGCGTTGGTGTGGAAGGGGGGGGGAACTTCTCCGACAGT ACCTGGAAAG	IS PIGHTHOHEWARFEAE KARWEERAELOAOVAFI OGERKGOENLKTDLVRRIK MEYALKOERAKTHKIKFO TDLNOGEKKADVSEOVSN GPVESVTLENSPLVWKEG ROLLROYLE
Shigella 1 ospB	prey67575	23	ATGGCAGCCTCCTT ACGGCTCCTCGGAGCTGCCTCCGGTCTCCGGTAGTGG 224 AGCCGGCGGCGGCAGCGGCACCGGCAGTTGCAGCGGTGTGTTCTAG GTCAGTGGCTTACAAGACTCCAGTTGGATTCATGGACTGGGCAAGGG GAATCCAATGGCAAAAATCTCATGAAACATGGCTACCCATTATATTATG ATGTGTTCCCTGATGCCTGCAAAGAGTTTCAAGATGCAGGTAGCA	MAASLRLLGAASGLRYWS RRLRPAAGSFAAVCSRSVA SKTPVGFIGLGNMGNPMAK NLMKHGYPLIIYDVFPDACK EFQDAGEQVVSSPADVAE

FORTESTOY OFFICE

				ATCTTCCCCAGCAGATGTTGCTGAAAAAGCTGACAGAATTATTACAATGCTGC	KADRIITMLPTSINAIEAYSG
				CCACCAGTATCAATGCAATAGAAGCTTATTATTATTATTATTATTATTATTATTATTATTATTA	DAYSKEI AKEVEKNOAVEM
				AAAAGI GAAGAAGGGCI CAI I AI I AAI AGAI I CCAGCACI AI I GAI CCIGCAG	DAPVOGGVGAABCANI TE
				TTTCAAAAGAAIIGGCCAAAGAAGIIGAGAAAAIGGGAGAGIIIICAIGGA	MYGGYEDEEAAAOELIGO
				GCCCC G C GG GG GG GG GG GCG GCG GG GG GCCCG GGGG GG GCCG GGGG GG GCCG GGGGG GCCG GGGGGG	MGSNVVYCGAVGTGOAAK
				TACATAGACTOCAACATAGTATACTATAGAACTATAGGAACTGGGACTGGGACTGGGACTGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGGACTGGGACTGGGAACTGGGGACTGGAACTGGGAACTGGGAACTGGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACA	ICNNMLLAISMIGTAEAMNL
				GCAAAGATCTGCAACAACATGCTGTTAGCTATTAGTATGGAACTGCTGA	GIRLGLDPKLLAKILNMSSG
				AGCTATGAATCTTGGAATCAGGTTAGGGCTTGACCCAAAACTACTGGCTAAA	RCWSSDTYNPVPGVMDGV
				ATCCTAAATATGAGCTCAGGACGGTGTTGGTCAAGTGACACTTATAATCCTGT	PSANNYGGGFGTTLMAKD
				ACCTGGAGTGATGGATGGCGTTCCCTCGGCTAATAACTATCAGGGTGGATTT	LGLAQDSATSTKSPILLGSL
				GGAACAACACTCATGGCTAAGGATCTGGGATTGGCACAAGACTCTGCTACCA	AHQIYRMMCAKGYSKKDF
				GCACAAAGAGCCCAATCCTTGGCAGTCTGGCCCATCAGATCTACAGGAT	SSVFQFLREEETF*
				GATGTGCAAAGGGCTACTCAAAGAAAGACTTCTCATCCGTGTTCCAGTTC	
Object	1	2002/2009	70	CIACGAGGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGG	AEEEEAEVROPKGPDPDSL
Singella	1	leyo, ooo		ACAGENTAGETTEACAGETTTATGGGGTATTGAACAGGGGGGGGAATGTCAT	SSOFMAYIEORRISHEGSP
adso				PONCOCITION OF A PROPERTY OF A PARTY OF A PA	VKPVAIREFOKTEDMRRYL
				ATATEAGAAGATACTTACATCAAAACAGGGTTCCAGCTGAGCATCTTCCCT	HONRVPAEPSSLLSLSASH
				COTOTOTO TO	NOLSHTDLELHORREQLVE
	•			CATCAGAGAGAGGAGTTAGTAGAGGGGAGAGAGAGAGAGA	RTRREAQLAALQYEEEKIR
				GCTGCCTGCAGTATGAGGAGGAGAAATAAGGACCAAGCAGATCCAGAGA	TKQIQRDAVLDFVKQKASQ
				GATGCTGTCCTGGACTTTGTCAAACAAAAGCATCACAAAAGTCCACAAAAAC	SPOKOHPLLDGVDGECPF
				AGCACCCGCTCCTAGATGGCGTAGATGGTGAGTGCCCCTTCCCATCCAGAA	PSRRSQHTDDSALCMSLS
				GGTCTCAGCACACTGATGATAGTGCCTTGTGCATGTCGCTGTCAGGGTTGAA	GLNQVGCAATLPHSSAFTP
	_	_		TCAAGTGGGCTGTGCTGCTACCCTGCCTCATTCTTCTGCCTTCACGCCTCTT	LKSDDRPNALLSSPATETV
				AAGAGTGATGACAGACCTAATGCTCTATTAAGTTCACCTGCAACAGAAACAG	HHSPAYSFPAAIQRNQPQR
				TTCATCATTCCCCTGCATATTCTTTCCTGCTGCTATCCAGAGAAATCAGCCT	<u> </u>
Shigella 1	٩	prey67637	25	ATGATACTACAGGAGTTACCAGATTTGGAGGAGCTCTTCCTGTGCCTTAATG 226	MILQELPDLEELFLCLNDYE
Baso				ACTATGAAACAGTGTCTTGTCCTTCTATTTGCTGTCATTCTCTTAAGCTACTAC	TVSCPSICCHSLKLLHII UN
_				ATATAACAGACAATAACCTCCAAGACTGGACTGAAATACGAAAGTTAGGAGTT	NLQDWTEIRKLGVMFPSLD
	-			ATGTTTCCTTCACTGGATACCCTCGTCCTGGCCAACAATCATTTGAATGCTAT	TLVLANNHLNAIEEPDDSLA
				TGAGGAGCCTGATGATTCATTGGCCAGGTTGTTTCCTAATCTTCGATCCATCA	RLFPNLRSISLHKSGLQSW
				GCCTCCACAAGTCAGGTTTGCAGTCCTGGGAAGACATTGATAAACTAAATTC	EDIDKLNSFPKLEEVRLLGI
				ATTTCCCAAACTGGAAGAAGTGAGATTGTTAGGAATTCCTCTTCTGCAGCCAT	PLLQPYTTEERRKLVIARLP
				ATACCACCGAGGAGCGAAGGAAATTGGTAATAGCCAGATTGCCATCAGTTTC	SVSKLNGSVVTDGEREDSE
	-			CAAACTTAATGGCAGCGTTGTTACTGATGGTGAACGAGAAGATTCTGAGAGA	RFFIRYYVDVPQEEVPFRY
				TTTTTTATTCGTTACTATGTGGATGTTCCACAGGAAGAAGTGCCATTCAGGTA	HELITKYGKLEPLAEVDLRP

ICOMSHEY DIELE

			TCATGAACTGATCACTAAATATGGGAAGTTGGAGCTTTGGCAGAAGTGGAC CTAAGACCCCAGAGCAGTGCAAAAGTAGAAGTCCACTTTAACGATCAGGTGG	QSSAKVEVHFNDQVEEMSI RLDQTVAELKKQLKTLVQL
			AAGAAATGAGCATTCGTCTGGACCAAACAGTGGCAGAACTAAAGAAACAGTT AAAAACTCTAGTACAATTACC	
Shigella 1 ospB	prey12713	56	AGTGGATGAGGTGCTGCAGATCCCCCCATCCCTGCTGACATGCGGGGGGTG 227 CCAGCAGAACATCGGGGACCGCTACTTCCTGAAGGCCATCGACCAGTACTG	VDEVLQIPPSLLTCGGCQQ NIGDRYFLKAIDQYWHEDC
			GCACGAGGACTGCCTGAGCTGCGACCTCTGTGGCTGCCGGCTGAGG	LSCDLCGCRLGEVGRRLYY
			TGGGGCGCCCTCTACTACAAACTGGCCGGAAGCTCTGCCGGAGAGAC	KLGHKLCHRDYLRLFGQD
			TATCTCAGGCTTTTTGGGCAAGACGGTCTCTGCGCATCCTGTGACAAGCGGA	GLCASCUKRIRAYEMTMRV
			TTCGTGCCTATGAGATGACAA GCGGGTGAAAGACAAAGTGTACGTGACAGATAC	CVGDBYL INSPINCEDDIX
			AT GETT FOR A GET	EWTKINGMI*
			AGATCAATGGATGATATAG	
Shigella 1	prey67836	27	CCTGAAGACAGCTGGCAAGTCTGAACCTTCCAGCAAGTTGCGAAAGCAACTT 228	LKTAGKSEPSSKLRKQLKK
ospB			AAAAAGCAGCAAGACTCTTTAGATGTCGTGGACTCTTCGGTCTCCTTTATG	QQDSLDVVDSSVSSLCLSN
			TCTGTCTAACACGGCATCATCTCATGGGACCAGAAAACTATTTCAGATTTATT	TASSHGTRKLFQIYSKSPFY
			CCAAATCTCCATTCTACCGAGCTGCCTCAGGTAATGAGGCCCTGGGAATGGA	RAASGNEALGMEGPLGQT
			AGGACCATTGGGCCAGACCAAATTCCTGGAAGACAAGCCTCAGTTCATCAGC	KFLEDKPQFISRGTFNPEK
			AGAGGAACCTTCAACCCGGAAAAGGGCAAACAAAATTAAAGAATGTGAAAA	GKOKLKNVKNSPOKTKETP
			ACTCACCTCAGAAAACCAAAGAGACCCCAGAGGGGACAGTCATGTCTGGCC	EGTVMSGRRKTVDPDCTS
			_	DON
Shigella 1	prey700	28	ATGGGAATTGGTCTTTCTGCTCAAGGTGTGAACATGAATAGACTACCAGGTT 229	MGIGLSAGGVNMNRLPGW
Bdso			GGGATAAGCATTCATATGGTTACCATGGGGATGATGGACATTCGTTTTGTTCT	DKHSYGYHGDDGHSFCSS
			TCTGGAACTGGACAACCTTATGGACCAACTTTCACTACTGGTGATGTCATTG	GTGQPYGPTFTTGDVIGCC
			GCTGTTGTTTATCTTATCAACAATACCTGCTTTTACACCAAGAATGGACAT	VNLINNTCFYTKNGHSLGIA
-			AGTITAGGTATTGCTTTCACTGACCTACCGCCAAATTTGTATCCTACTGTGGG	FTDLPPNLYPTVGLQTPGE
			GCTTCAAACACCAGGAGAAGTGGTCGATGCCAATTTTGGGCAACATCCTTTC	VVDANFGQHPFVFDIEDYM
			GTGTTTGATATAGAAGACTATATGCGGGAGTGGAGAACCAAAATCCAGGCAC	REWRTKIQAQIDRFPIGDR
			AGATAGATCGATTTCCTATCGGAGATCGAGAGGAGAATGGCAGACCATGAT	EGEWQTMIQKMVSSYLVH
		_	ACAAAAATGGTTTCATCTTATTTAGTCCACCATGGGTACTGTGCCACAGCAG	HGYCATAEAFARSTDQTVL
			AGGCCTTTGCCAGATCTACAGACCAGACCGTTCTAGAAGAATTAGCTTCCAT	EELASIKNRORIOKLVLAGR
			TAAGAATAGACAAAGAATTCAGAAATTGGTATTAGCAGGAAGAATGGGAGAA	MGEAIETTQQLYPSLLE
			GCCATTGAAACAACACACAGTTATACCCAAGTTTACTTGAAAG	
Shigella 1	prey67844	83	TTCCATACAGGAACCCCATCTGAAGGTCACCAACATCAAAGACCAAAGGTAG 230	FHTGTPSEGHQHQRPKVD
gdso			ATAAATCCACGAAGTTGAGGAAAAACCAGTGCAAAAAGGCTGAGAATTCCAA	KSTKLRKNQCKKAENSKN
			AAACCAGAAAGGCTCTTCTCCTCCAAAGGATCAAAACTCCTCGCCAGCAAGG	QKGSSPPKDQNSSPAREQ
			GAACAAAACCAGATGGAGAATGAGTTTGATGAATTGACAGAAGTAGGCTTCA	NOMENEFDELTEVGFRRW
			GAAGGTGGGTAATAACAAGTAAGCTAAAGGAGCATGTTCTAACCCAATGCAA	VITSKLKEHVLI OCKEVKNL
			GGAAGT AAGAACCT GAAAAAGGT ATG	ENHL

HOTTO, VOTITOR

Shinella		prov67853	30	PACCETAGACAGATAGAGATACCAGACCTCACCTCAGGAGGCATGGAAGTACCA 231	AVDGEGAGI TSFAWKYOV
ospB			3		TSHREDRFPLSSRLRLALK
				GCACTGAAGAATCTTGGTGCTGACAGACACAGAGCAGGGTCTCTCGTGGAA	NLGADRHRAGSLVEQELS
				CAGGAGTTGTCTGGTCTGTTCAGTTTGATGAGTGGCAGAAAATGAGACGATG	GLFSLMSGRK*DDGKCVC
				\neg	GPXFXCXGX
Shigella	-	prey66272	3	ATGTGGGCCCTGGGTCAAGCAGGTTTTGCCAACCTCACCGAGGGACTGAAA 232	MWALGGAGFANLTEGLKV
ospB				GTGTGGCTGGGGATCATGCTGCTGTGCTGGGCATCAAGTCTCIGTCTCCC	WLGIMLPVLGIKSLSPFAIIY
				TTTGCCATCACATACCTGGATCGGCTGCTCCTGATGCATCCCAACCTTACCA	LDRLLLMHPNLTKGFGMIG
				AGGGCTTCGGCATGATTGGCCCCAAGGACTTCTTCCCACTTCTGGACTTTGC	PKDFFPLLDFAYMPNNSLT
				CTATATGCCGAACAACTCCCTGACACCCCAGCCTGCAGGAGCAGCTGTGTCA	PSLQEQLCQLYPRLKVLAF
				GCTCTACCCCCGACTGAAAGTGCTGGCATTTGGAGCCAAAGCCGGATTCCAC	GAKPDSTLHTYFPSFLSRA
				CCTGCATACCTACTTCCCTTCTTTCCTGTCCAGAGCCACCCCTAGCTGTCCC	TPSCPPEMKKELLSSLTEC
				COTGAGATGAAGAAGAGCTCCTGAGCAGCCTGACTGAGTGCCTGACGGTG	LTVDPLSASVWRQLYPKHL
				GACCCCCTCAGTGCCAGCGTCTGGAGGCAGCTGTACCCTAAGCACCTGTCA	SQSSLLLEHLLSSWEQIPKK
				CAGTCCAGCCTTCTGCTGGAGCACTTGCTCAGCTCCTGGGAGCAGATTCCC	VQKSLQETIQSLKLTNQELL
				AAGAAGGTACAGAAGTCTTTGCAAGAAACCATTCAGTCCCTCAAGCTTACCA	RKGSSNNQDVVTCDMACK
				ACCAGGAGCTGCTGAGGAAGGGTAGCAGTAACAACCAGGATGTCGTCACCT	GLLQQVQGPRLPWTRLLLL
				GTGACATGGCCTGCAAGGGCCTGTTGCAGCAGGTTCAGGGTCCTCGGCTGC	LLVFAVGFLCHDLRSHSSF
				CCTGGACGCGGCTCCTCCTGTTGCTGCTGGTCTTCGCTGTAGGCTTCCTGT	QASLTGRLLRSSGFLPASQ
				GCCATGACCTCCGGTCACACACCTCCTTCCAGGCCTCCCTTACTGGCCGGT	QACAKLYSYSLQGYSWLG
				TGCTTCGATCATCTGGCTTCTTACCTGCTAGCCAACAAGCGTGTGCCAAGCT	ETLPLWGSHLLTVVRPSLQ
				CTACTCCTACAGTCTGCAAGGCTACAGCTGGCTGGGGGAGACACTGCCGCT	LAWAHTNATVSFLSAHCAS
				CTGGGGCTCCCACCTGCTCACCGTGGTGCGGCCCAGCTTGCAGCTGGCCT	HLAWFGDSLTSLSQRLQIQ
				GGGCTCACACCAATGCCACAGTCAGCTTCCTTTCTGCCCACTGTGCCTCTCA	LPDSVNQLLRYLRELPLLFH
				CCTTGCGTGGTTTGGTGACAGTCTCACCAGTCTCTCAGAGGCTACAGATC	QNVLLPLWHLLLEALAWAQ
				CAGCTCCCCGATTCCGTGAATCAGCTACTCCGCTATCTGAGAGAGCTGCCC	EHCHEACRGEVTWDCMKT
				CTGCTTTTCCACCAGAATGTGCTGCTGCCACTGTGGCACCTCTTGCTTG	QLSEAVHWTWLCLQDITVA
				CCCTGGCCTGGGCCCAGGAGCACTGCCATGAGGCATGCAGAGGTGAGGTG	FLDWALALISQQ*
				ACCTGGGACTGCATGAAGACACAGCTCAGTGAGGCTGTCCACTGGACCTGG	
				CTTTGCCTACAGGACATTACAGTGGCTTTCTTGGACTGGGCACTTGCCCTGA	
Shinella	٥	Drev700	3	ATGGGAATTGGTCTTTCTGCTCAAGGTGTGAACATGAATAGACTACCAGGTT 233	MGIGLSAQGVNMNRLPGW
ospD1	ı	22.62.4	!		DKHSYGYHGDDGHSFCSS
				TCTGGAACTGGACAACCTTATGGACCAACTTTCACTACTGGTGATGTCATTG	GTGQPYGPTFTTGDVIGCC
				GCTGTTGTGTTAATCTTATCAACAATACCTGCTTTTACACCAAGAATGGACAT	VNLINNTCFYTKNGHSLGIA
				AGTTTAGGTATTGCTTTCACTGACCTACCGCCAAATTTGTATCCTACTGTGGG	FTDLPPNLYPTVGLQTPGE
				GCTTCAAACACCAGGAGAAGTGGTCGATGCCAATTTTGGGCAACATCCTTTC	VVDANFGQHPFVFDIEDYM
				GTGTTTGATATAGAAGACTATATGCGGGAGTGGAGAACCAAAATCCAGGCAC	REWRTKIQAQIDRFPIGDR
				AGA I AGA I CGA I I CC I A I CGGAGA GAGAGAGA I GGCAGACCA I GA I	EGEWQ! MICHWINSSTLVF

TOOKERDY OUTTOO

				ACAAAAAATGGTTTCATCTTATTTAGTCCACCATGGGTACTGTGCCACAGCAG AGGC	НGYCATAE
	a	prey2492		TIGGGAAAGGGGTCTAGAGAGAGAGTGAGGGGAGCTGGGCCTA TGTCAAAAGGGGGTCTCAGTACAGAGAGAGTGAGGGATCCTGGCGCCTCCAGGC TGTCAAAAGGCGGTCTCAGTACAGAGAGAAAGTTGAGAGAGCACTCTCAGCC TTGCATCAAAACTTAGAAAGTTGAAAAAGTAGAAAATTCCAAAAACTTAGAAAACTTAGAAAGTTTCAAAGAAGTTTCAAAGAATTTTCAAAGAATTTTCAAAAAACTTAGAAAGATTTCAAAGAATTTTCAAAGAATTTTCAAAGAATTTTCAAAGAATTTTTCAAAGAATTTTTCAAAGAATTTTTCAACAATTTTCAACAATTTTCAAAAATTTTCAAAAATTTTCAAAAACTTTAGATTAGATTTCAATTATTCAATTATTATTTAT	THUKROAMKSEGSLAVYK GGLSTFEADALSAHOK LEADGTEKVEGSMTOKLEN UNRASNTADTI-CQULGA KUNRASNTADTI-CQULGA KOKAGSTRAALINUCARFK INDYEKKSLEATENOKADTOV INDYEKKSLEATENOKADTOV INDYEKKSLEATENOKADTOV INDYEKKSLEATENOKADTOV INDYEKKSLEATENOKADTOV INGLATENOKATION INGLATENOKATION INGLATENOKATION INGLATENOKATION INGLATENOKATION INGLATENOKATION INGLATENOKATION INGLATORIUCATION INGLATORI
Shigella ospD1	CI .	prey67651	34	CAGTATARGARGCCTTRGARGARTGARGARTGAGGGAAATTGAGGGGAATTGAGGGCACACC 2335 CAGGAGCTGATAAAGCAGAAAAAAAGAGTATACAGTTAAGCTCANUCCC AGGAGCTGATAAGAGGAGAAACAACTAGAATATACAAAAGAGAATGGTT CTCAACGTAGGAGCGACAAAGAACATGATACAACAAGAGAGATGGTT CAGAGGTAGGAGCGACAAAAGAACATGAGAGCTGTAAAAGAAGTTGAAAAGAGTTTGAAGAGTGTTTGAGAGCTGTTAGAACATTGAAAAGTTGAAAAGTTTTTGAAGATTTACAACAACTGAGATTTAAAAAGAGTGTTTTGAACAACTTAACAACTGAGA	QYKKALENETNEEKSGTPG ADKAEKRYKTVKLXPVSL YSSHEATRIYKENGSKORRS EKRT-S-NURPSFRGKNKI R-SCMQNLKSLMSXKKSVS DLQQLX

TOOHUMBY OILION

					450111111111111111111111111111111111111
Shigella ospD1	N	prey67653	35	CCCTGAAATCTGCAAAATGGCTGATAATTTGGATGAATTTATTGAAGAGGAAA 236 AAGCCAGATTGGCCGAAGACAAGCAGAGTTGGAAAGTGATCCACCTTACAT	PEICKMADNLDEFIEEGKAR LAEDKAELESDPPYMEMK
				GGAAATGAAGGGAAAGTTGTCAGCGAAGCTTTCTGAAAACAGTAAGATACTG	GKLSAKLSENSKILISMAKE NIPPNSOOTBGSI GIDYGI
				CCTTAGGAATTGATTATGGATTAAGTTTACCACTTGGAGAAGACTATGAACGG	SLPLGEDYERKHKLKEEL
					1
	2	prey67667	98	CGACCAGGGCACACCCCAGTACATGGAGAGCATGGAGCAGGTGTTTGAGCA 237	DOG! POYMENMEDVFECO
ospD1				GTGCCAGCAGIICGAGGAGAAACGCCIICGCIICIICCGGGAGGIICIGCI	
				GGAGGTTCAGAAGCACCTAAACCTGTCCAATGTGGCTGGTTACAAAGCCAII	KHLNLSNVAGYKAIYHDLE
				TACCATGACCTGGAGCAGAGCATCAGAGCAGCTGATGCAGTGGAGGACCTG	QSIRAADAVEDLHWFHANH
				AGGTGGTTCCGAGCCAATCACGGGCCAGGCATGGCCATGAACTGGCCGCA	GPGMAMNWPQFEEWSAD
				GTTTGAGGAGTGGTCCGCAGACCTGATTCGAACCCTCAGCCGGAGAGAA	LIRTLSRREKKKATDGFTLT
				GAAGAAGGCCACTGACGGCTTCACCCTGACGGGCATCAACCAGACAGGCGA	GINQTGDQFLPSKPSS
Shigella	2	prey67657	37	CCCGCCTGCCATGGACTGGATCTTCCAGTGCATCTCCTACCATGCCCCCGA 238	PPAMDWIFQCISYHAPEAL
ospD1				GGCTCTGCTGACCGAGATGATGGAAAGGTGTAAGAAACTAGGAAACAATGC	LTEMMERCKKLGNNALLLN
				CTTGCTGTTGAATTCTGTGATGTCTGCCTTCCGGGCTGAGTTCATCGCCACA	SVMSAFRAEFIATRSMDFIG
				AGGTCTATGGATTTCATTGGCATGATTAAAGAGTGTGATGAATCTGGTTTCCC	MIKECDESGFPKHLLFRSL
				CAAGCATCTTCTTTCGATCACTGGGATTAAACTTGGCCTTGGCTGATCCTC	GLNLALADPPESDRLQILNE
				CTGAGAGTGACCGACTTCAGATTCTCAACGAAGCTTGGAAAGTCATCACTAA	AWKVITKLKNPQDYINCAE
				GCTGAAGAACCCACAGGACTACATTAATTGTGCCGAAGTGTGGGTGG	VWVEYTCKHFTKREVNTVL
				ACCTGCAAGCATTTCACGAAACGAGAGGTGAATACCGTTTTGGCAGATGTCA	ADVIKHMTPDRAFEDSYPQ
				TCAAGCACATGACTCCAGATCGTGCATTTGAAGATTCCTACCCCCAGCTTCA	LQLIIKKVIAHFHDFSVLFSV
				GTTAATAATTAAGAAAGTTATTGCCCACTTCCATGACTTCTCAGTTCTTTTCTC	EKFLPFLDMFQKESVRVEV
				AGTGGAAAAATTTCTGCCGTTTCTGGACATGTTCCAAAAAGAGAGTGTGCGG	CKCIMDAFIKHQQEPTKD
				GTGGAGGTTTGCAAATGCATCATGGACGCCTTTATCAAGCATCAACAAGAGC	
				CCACCAAGGACC	
Shigella	N	prev67501	38	CTTCCGCCTGGAACAGCTGGAATGCCTTGATGATGCAGAAAAAAAA	FRLEGLECLDDAEKKLNLA
ospD1		,		TTGGCCCAGAAATGCTTTAAAAATTGTTACGGAGAAAATCATCAGAGACTGGT	OKCFKNCYGENHORLVHIK
				CCACATAAAAGGAAATTGTGGGAAAGAGAAGGTACTGTTTCTAAGACTCTAC	GNCGKEKVLFLRLYLLQGI
				TTACTTCAAGGGATCCGAAACTATCACAGTGGAAATGATGTAGAGGCTTATG	RNYHSGNDVEAYEYLNRH
				AGTATCTTAACAGGCACGTCAGCTCTTTAAAGAGCTATATATTGATCCATCAA	VSSLKSYILIHQKWTICCSW
				AAGTGGACAATTTGTTGCAGTTGGGGTTTACTGCCCAGGAAGCACCGGCTTG	GLLPRKHRLGLRACDGNV
				GCCTGAGGGCGTGTGATGGGAACGTGGATCATGCGGCCACTCATATTACCA	DHAATHITNRREELAQIRKE
				ACCGCAGAGAGGAACTGGCCCAAATAAGGAAGGAGGAAAAAAAA	EKEKKRRRLENIRFLKGMG
				GACGCCCCTCGAGAACATCAGGTTTCTGAAAGGGATGGGCTACTCCACGC	YSTH
				-	
Shigella	2	prey67678	33	GAACAAGCTGAGGGTGTTGGACCCAGAGGTTACCCAGCAGACCATAGAGGT 240	OKDEVDDPEVTOQTIELKEE CKDEVDKIGOFOKIVGGLIE
OsbO					

RODFBF87 DILIPOR

			*O	A CHANTER AND A CONTRACTOR
			G GG GG AA GAGC G GA CAAC GCAAAAGAAAG	BNI I KSIAKOBFAOOOOI O
-			AAAGA GAAGGCCA CGG GC GC GCGAACT GCGCAATAGCAAAAAAAAAA	ALIAEKKMOLERYRVEYEA
			AGCTAGAAAGGTATCGGGTTGAATATGAAGCTTTGTGTAAAGTAGAAGGAAAGAAA	LCKVEAEQNEFIDQFIFQK*
Shigella 2	prey67578	40	ATGGCGGTGGAGACTCTGTCCCCGGACTGGGAGTTTGACCGCGTTGACGAC 241	MAVETLSPDWEFDRVDDG
ospD1			GGCTCGCAGAAAATTCATGCCGAAGTCCAACTTAAGAATTATGGGAAATTTCT	SOKIHAEVOLKNYGKFLEE
			TGAGGAGTATACCTCTCAACTGAGAAGAATTGAGGACGCTCTGGATGACTCA	YTSQLRRIEDALDDSIGDV
			ATTGGAGATGTTTGGGATTTCAATCTTGATCCTATAGCATTAAAGCTTTTGCC	WDFNLDPIALKLLPYEQSSL
			TTATGAACAGTCCTCTTTTGGAACTCATAAAGACTGAAAACAAGGTCTTAA	LELIKTENKVLNKVITVYAAL
			ACAAAGTCATCACTGTTTATGCTGCACTTTGTTGTGAAATCAAGAAATTAAAAT	CCEIKKLKYEAETKFYNGLL
			ATGAGGCTGAAACTAAAATTTTACAATGGTCTCTTGTTTTATGGAGAAGGAGCT	FYGEGATDASMVEGDCQI
			ACAGATGCCAGCATGGTGGAAGGTGATTGCCAAATTCAAATGGGGGAGATTTA	QMGRFISFLQELSCFVTRC
			TTTCATTCTTACAGGAACTGTCTTGCTTTGTTACGAGGTGCTATGAAGTGGTG	YEVVMNVVHQLAALYISNKI
			ATGAACGTAGTCCACCAGTTGGCTGCCTCTATATCAGTAACAAGATTGCAC	APKIIETTGVHFQTMYEHLG
			CCAAAATTATAGAGACAACTGGAGTTCATTTTCAGACTATGTATG	ELLTVLLTLDEIIDNHITLKD
			GGAGAACTGCTAACAGTTTTGCTCACCCTGGATGAAATTATTGATAATCATAT	HWTMYKRLLKSVHHNPSK
			CACACTGAAAGACCACTGGACTATGTACAAAAGGTTACTGAAATCTGTCCAT	FGIQEEKLKPFEKFLLKLEG
			CACAATCCTTCAAAATTTGGAATTCAGGAAGAAAAATTAAAAGCCATTTGAAAA	QLLDGMIFQACIEQQFDSL
		_	GTTCTTGCTGAAGCTAGAAGGGCAATTACTGGATGGAATGATATTCCAGGCC	NGGVSVSKNSTFAEEFAHS
			TGTATAGAACAACTTTGATTCTCTCAATGGAGGAGTATCTGTGTCAAAAAA	IRSIFANVEAKLGEPSEIDQ
			TAGTACTTTTGCTGAGGAATTTGCACATAGTATTCGGTCAATTTTTTGCAAATG	RDKYVGICGLFVLHFQIFRT
			TAGAAGCCAAACTTGGAGAACCTTCTGAAATTGACCAGAGAGAG	IDKKFYKSLLD
			TGGAATTTGTGGACTCTTTGTATTGCACTTTCAGATTTTTCGAACTATTGATAA	
			AAAGTTTTATAAGTCTTTATTGGAC	
Shigella 2	prey67580	14	GCACTCCCCGCCGCTCCGACTCCGCATCTCTGTCCGCTCCCTGCACTCAG 242	TPRRSDSAISVRSLHSESS
ospD1			AGTCCAGCATGTCTCTGCGCTCCACATTCTCACTGCCCGAGGAGGAGGAGG	MSLRSTFSLPEEEEPEPL
			AGCCGGAGCCACTGGTGTTTGCGGAGCAGCCCTCGGTGAAGCTGTGCTGTC	VEAEQPSVKLCCQLCCSVE
		_	AGCTCTGCTGCAGCGTCTTCAAAGACCCCGTGATCACCACGTGTGGGCACA	KDPVITTCGHIFCHRCALK
			CGTTCTGTAGGAGATGCGCCTTGAAGTCAGAGAGTGTCCCGTGGACAACG	SEKCPVDNVKLTVVVNNIA
			TCAAACTGACCGTGGTGGTGAACAACATCGCGGTGGCCGAGCAGATCGGGG	VAEQIGELFIHCRHGCRVA
			AGCTCTTCATCCACTGCCGGCACGGCTGCCGGGTAGCGGGGCAGCGGGAAG	GSGKPPIFEVDPRGCPFTIK
			CCCCCCATCTTTGAGGTGGACCCCCGAGGGTGCCCCTTCACCATCAAGCTC	LSARKDHEGSCDYRPVRC
			AGCGCCCGGAAGGACCACGAGGCCAGCTGTGACTACAGGCCTGTGCGGTG	PNNPSCPPLLRMNLEAHLK
			TCCCAACAACCCCAGCTGCCCCCCGCTGCTCAGGATGAACCTGGAGGCCCA	ECEHIKCPHSKYGCTFIGN
			CCTCAAGGAGTGCGAGCACATCAAATGCCCCCACTCCAAGTACGGGTGCAC	QDTYETHLETCRFEGLKEF
			GTTCATCGGGAACCAGGACACTTACGAGACCCACCTGGAGACTTGCCGCTT	LOQTDDRFHEMHVALACK
			CGAGGGCCTGAAGGAGTTTCTGCAGCAGACGGATGACCGCTTCCACGAGAT	DOEIAFLRSMLGKLSEKID
			GCACGTGGCTCTGGCCCAGAAGGACCAGGAGATCGCCTTCCTGCGCTCCAT	

HODELFRY OFFICE

				GCTGGGAAAGCTCTCGGAGAAGATCGACC	
Shigella ospD1	Ø	prey3160	42		RKLHELTVMQDRREQARQ DLKGLEETVAKELQTLHNL RKLFVQDL
Shigella ospD1	a	prey50427	84	ATGGGGGGTTTGGAAAAGTGTTGGAAAGGTTGGAAAGAGGGGGAAGAGGAAGGAAGGAAGGAAGAGGGGGG	LSTESFLANDAS LSTESFLANDAS LSTESFLANDESISIRFH VAUSPLUNIEGREMODE KOKALDVEARKONDEKKAL LTRVGELDNVONRKAPNA LTRVGELDNVONRKAPNA SDDOWWENTETVYSNSEVR NLINPATFPNSFPSHTEHS NLINPATFPNSFPSHTEHS CDSSNISHVENEAFFRSPG CDSSNISHVENEAFFRSPG ARCHEVIPPPYWASLONL NEKSKEYTERCSRSSLR OLLAEUNPDYWASLONL NEKSKEYTERCSRSSLR SWMRYNUESHLDKEHDAVE VADCYKEKGOLTGKHOVS VATGHOVNUKSNILOGAST CASSMSMPVASFSKVDFI VTENNYKSLTGSVAKLPSP
Shigella ospD1	α	prey63765	44	GRACAGECCAACCTCTGGCAACCAGGGGTTACCAAGCTGCAACTGCAACC GGCCAAACCAAGGTGGAACCAGGGGTTACCAAGTTGCACCAAGCTGGCAA GGGCCAAACCAAGGAGTACCTTGGAACAAGTTGACCAAGCTGGCAA GGGCCAAACCAAGGATACCTTCCACTTGGAAGATTCTCAAACAGCTGCAA ACTCAGGATTGTGGACACCACTTCACTT	SEPS GARPA (STR. LTAAAF KPVGSTGVIKSPSWORPN GGVPSTGAISNSATVSGSV AANSALGGYTPSDODTLV GRAEHPAGKGTTPMCAHC GNONFGPETVALGKSWHPE EFNCAHCKNTMATGFVEE KGALYCELCYEKFFAPEGG KGALYCELCYEKFFAPEGG KGALYCELCYEKFFAPEGG COPRICERIVALKGTWH VSCFVCVACGKPIRALKGTWH LEDGEPYCETDVYALFGTI CHOCEFPICAGUMINVFH LEDGEPYCETDVALFGTI OHOCEFPICAGUMINVFH LEDGEPYCETDVALFGTI

HODISTRY DIFFIOR

			TOAAAACTOTOTOTOTATOTTTCCCTTC.C.CT.CCCTCC.C.TCCCC	COTEESKYDKBI CKKHAHS
			GGGCI ACACCI GGCAI GACACI GCI I GGIA GCI CACI GGIA GGIA	VNF*
Shigella 2 ospD1	prey67623	45	ATTITATAGGAGGGATACACCATACATGGTACAGCCACAGTACCGAATCTAT 246 GAGATGAACAGAGTGCAGTTCOACACAGGAGATATAGACACATCATGG TOGAAACACACATGAATTITTAAACATGACGCACATTAACCTTTG	FYRRHTPYMVQPEYRIYEM NKRLQSRTEDSDNLWWDA FATEFFEDDATI TI SFCLED
			ATTITGITTGGAAGATGGACCAAAGCGATACACTATCGGCAGGACCCTCATC	GPKRYTIGRTLIPRYFSTVF
			CCCCGTTACTTTAGCACTGTGTTTGAAGGAGGGGTGACCGACC	EGGVTDLYYILKHSKESYH
			TTCTCAAACACTCGAAAGAGTCATACCACAACTCATCCATC	PMFTKVCTEGRULEFTFDD
			ATGTACAGAAGGCAGACTGATCTTGGAGTTCACCTTTGATGTCATGAGA	LMRIKTWHFTIRQYRELVP
			ATCAAAACATGGCACTTTACCATTAGACAATACCGAGAGTTAGTCCGGAGAA	RSILAMHAQDPQVLDQLSK
			GCA CC AGCCA GCA GCACAAGA CC CAGG CC GGA CAGC G CCAA	I EPMOEL MSRHKTYNLSPR
			TGTGTAATATTGGAGCCAATGCAGGAACTGATGTCGAGACATAAAACTTACA	DCLKTCLFQKWQRMVAPP
			ACCTCAGTCCCCGAGACTGCCTGAAGACCTGCTTGTTTCAGAAGTGGCAGA	AEPTRQP
			\neg	CT SYTHOGON OF THE CONTROL OF THE CO
Shigella 2	prey7315	46	ATGCTGGATAGGGATGTGGGCCCAACTCCCATGTATCCGCCIACAIACCIG 24/	MLDHUVGP I PMYPP I YLEP
ospD1			GAGCCAGGGATTGGGAGGCACACACACATTGGCAACCAAACTGAGA	GIGHHI PYGNOI DYRIFEL
			ATATTTGAGCTTAACAAACGGCTTCAGAACTGGACAGGAGGAGIGIGACAATC	NYHECON PECCENTWWD
			TCTGGTGGGATGCAIICACGACIGAGIICIIIGAGGAIGAIGACAIGIIGAC	DODKOVTIGETI IDDVCDCI
			CALCACITICIGCCIGGAGGAIGGACCAAAGAAAAINIAACATIGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	FEGGATEI YYVI KHPKFAF
			C GA CCCACGCACGCACCACCACCACCACCACCACCACCACCAC	HSNEVSI DCDOGSMVTCH
			TACLATETICT FAGGAGGAGGAGGAGGAGGAGGAGGAGCATGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	GKPMFTQVCVEGRLYLEF
		_	CCCAGGTGTGTGTGTGGAGGGCCGGTTGTACCTGGAGTTCATGTTTGACGACA	MFDDMMRIKTWHFSIRQH
			TGATGCGGATAAAGACGTGGCACTTCAGCATCCGGCAGCACCGAGAGCTCA	RELIPRSILAMHAQDPQML
		_	TOCCCCGCAGCATCCTTGCCATGCATGCCCAAGACCCCCAGATGTTGGATC	DOLSKNITRCGLSNSTLNYL
			AGCTCTCCAAAAACATCACTCGGTGTGGGCTGTCCAATTCCACTCTCAACTA	RLCVILEPMQELMSRHKTY
			CCTCCGACTCTGTGTGATACTCGAGCCCATGCAAGAGCTCATGTCACGCCAC	S
ollonido.	100 ZEO 4	127	ANGTONOTROCTTON ACCOUNTS AND	VTASTTCEKLEKARNELGT
		<u>-</u>	CAAACAGTGTATGAAGCATTCGTCCAGCAGCACCAGGCTGAAAAAAAA	VYEAFVQQHQAEKTEREN
		_	GAGAGAATCGGCTTAAAGAGTTTTACACCAGGGAGTATGAAAAGCTTCGGGA	RLKEFYTREYEKLRDTYIEE
			CACTTACATTGAAGAAGCAGAGAAGTACAAAATGCAATTGCAAGAGCAGTTT	AEKYKMOLOEOFDNLNAA
			GACAACTTAAATGCTGCGCATGAAACCTCTAAGTTGGAAATTGAAGCTAGCC	HETSKLEIEASHSEKLELLK
			ACTCAGAGAAACTTGAATTGCTAAAGAAGGCCTATGAAGCCTCCCTTTCAGA	KAYEASLSEIKKGHEIEKKS
		-	AATTAAGAAAGGCCATGAAATAGAAAAGAAATGCGCTTGAAGATTTACTTTCG	LEDLLSEKGESLEKGINDLK SENDAI NEKI KSEEOKBBA
		_	AGAAGCAGGAA CGCTAGAGAAGCAAA CAATGATCTGAAGAGTGAAAATGA	SEINDALINERLINGLESSIN III IN

MODWARD, GILLE

					REKANLKNPOMYLEGELE SLKAVLENKEKHPODINL MKNEKLYODNITALVDKLKP FOGENEELKARMDKHMAIS FOLSTEGAVLOESLEKEK VNKRLSMENEELLWKLHW GDLCSPKRSPTSSAIPLOS PRNSGSFPSPSISPF*
Shigelia ospD1	N	prey53735	48	GAAGCTGCTGCTAGATCAGGCAGCAGCAGAGGCGGGTTGAAT (249 GAAGCTGCTGCTGGGCTGAATCAGCCAGCACACAGAGCCGGTTGAAT (249 GGGGGAACCCCTGGGGCTGCGTGCTGCGCACACACTGGTGCAGGCGGTTTGGAGCCGTTTGGGGGGAGCCGAGCCAGGCTGGTGTGTGGGCTGGAGCCGAGTTGGGGCGAGTTTGGAGCCAGTTTGGAGCCAGTTTGGAGCCAGTTGCGAGCCAGTTGCGAGCCAGTTGCAGGCCAGTTGCAGGCCAGTTCCAGGCCAGTTCCAGTGCCAGCTGCCAGGCCAGTTCCAGTTCCAGTTCCAGGCCAGTTGCAGCGCAGCAGCAGTTCCAGTGCGCAGCTGCCAGGAGCAGTTGCAGCGCAGCAGCAGTTAGCAGCGCACTGCAGGAGCAGTTGGAGACGCAGCAGTTGGAGACGCCAGAAGGAGCAGTTGAATCAGCTGGGCCAGTTGGAGACGCTCGCAGAAGGAGCCAGTAACGCCAGTTGAGAACTTCTGCAGAGCCATAACGCCGTTGCAGAAATGCCATTTGAGTTGCAGCGCCATAACGCAAAATGCCATTTGAGTTGCAGCAGCTTGCAAAATGCCATTTGAGTTGCAGCAGCTTGCAAAATGCCATTTGAGTTGCAGCAGCTTGCAAAATGCCATTTGAGTTGCAGTTGCAGAGCTTGCAAAATGCCATTTGAGTTGCAGTTGCAAAATGCCATTTGAGTTGCAACTGCAAAATGCCATTTGAGAGCTTGCAAAATGCCATTTGAGCAGCAAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGAAATGCCATTTGAGCCAAAATGCCAAAAATGCCAATAACAAAAATGCAAATGCAAATGCAATGCACAAAATGCCAAAAATGCAAAAATGCAAAAATGCAAAAAATGCAAAAATGCAAAAATGCAAAAATGCAAAAATGCAAAAAATGCAAAAAATGCAAAAATGCAAAAATGCAAAAATGCAAAAAATTGAGAAAAAAAA	SLPPSTGTAGASHIVA AGUNGATELVOASHGT OD ARASGREGODFSTELE AGVERMAGOAPSCENDENACY (SNLYGISMSSKILLAARA ATTOSINGLITMOTOCAPG OKECDNALRELETVRELLE NOVORINOMSYGEGLDSVM GON PETGOAPG OKECDNALRELTVRELLE OKECDNALRELTVRELLE OKECDNALRELTVRELLE OKECDNALRELTVRELLE OKECDNALRETVRELLC OKECDNALRETVRELC OKECDNALRETVRELC OKECDNALRETVRELC OKECDNALRETVRENT OKAGNAC OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKUSDNA OKAGOGGLEPTOFARAN OKUSDNA OKUSD
Shigella ospD1	N	prey67630	64	GAGGACCTGCAGCCAGCGCCCTGAGGCCCTTCAACAAGCTC 250 GCTGGCTCTGAACAACCCCGCGTGTGATCAGGATTAGCACTTCACCTGGGCGC AGGGCCCTTCAACAACTCCCGCTAGTTGAGCCACAAGGATTAACGTCCAAGAACTCCCGGGCC AGGGCCCTTTGTCTCAACAACTCCCGCTATTAAGCATTAACCTGGT TGTATCCATTGTCTCAACAACCATCATGAACTATCAGTACCGGT AGTGTCCCACCCCATGCTGTATGAACTATGACTTAGCCTTAACAAG AATCCAAGGACCAAAGCCCTTGTTCTTAAAGGTTTGTGGAA	EDLQPPSALSAPFTNSLAR SARQSVLRYSTLPGRRALK NSRLVSQKDDVHVCILCLR AIMNYQYGFNLVMSHPHAV NEELSLNNKNPRTKALVLE LLA

TODIUS STATES

	2	prey12665	20	GAAGCGGCACGAGCGAATGATCAAGAACCGGGAGTCAGCCTGCCAGTCCC 251	KRHERMIKNRESACOSRR KKKEVI OGI EARI DAVI AD
ındso				TACTGGCTGACAACCAGCTCCGCCGAGAATGCTGCCCTCCGGCGGC	NOOLRRENAALRREALL
				GGCTGGAGGCCCTGCTGGCTGAAACAGCGAGCTCAAGTTAGGGTCTGGAA	AENSELKLGSGNRKVVCIM
				ACAGGAAGGTGGTCTGCATCATGGTCTTCCTTCTTCATTGCCTTCAACTTT	VFLLFIAFNFGPVSISEPPSA
				GGACCTGTCAGCATCAGTGAGCCTCCTTCAGCTCCCATCTCTCCTCGGATGA	PISPRMNKGEPOPRRHLLG
				ACAAGGGGAGCCTCAACCCCGGAGACACTTGCTGGGGTTCTCAGAGCAAG	FSEQEPVOGVEPLOGSSQ
				AGCCAGTTCAGGGAGTTGAACCTCTCCAGGGGTCCTCCCAGGGGCCCTAAGG	GPKEPQPSPTDQPSFSNLI
				AGCCCCAGCCCACACACACACCCAGTTTCAGCAACCTGACAGCCT	AFPGGAKELLLRDLDQLFL
				TCCCTGGGGGCGCCAAGGAGCTACTACTAAGAGACCTAGACCAGCTCTTCC	SSDCRHFNRTESLRLADEL
				TCTCCTCTGATTGCCGGCACTTCAACCGCACTGAGTCCCTGAGGCTTGCTGA	SGWVQRHQRGRRKIPQRA
				CGAGTTGAGTGGCTGGGTCCAGCGCCACCAGAGAGGCCGGAGGAAGATCC	QERQKSQPRKKSPPVKAV
				CTCAGAGGGCCCAGGAGAGACAGAAGTCTCAGCCACGGAAGAAGTCACCTC	ā
				$\overline{}$	1000
	2	prey67631	5	TGAGAGCGAGGTCTCGGAGCATCTCAGTGCCAGCTCGGCTTCTGCCATCCA 252	ESEVSEHLSASSASSIQUE
l OspD1				GCAGGACAGCACTTCCAGCATGCAGCCACCATCTGAAGCCCCCATGGTGAA	STSSMOPPSEAPMVNIVS
				CACAGTCAGCTCAGCTTATTCGGAGGATTTTGAAAACTCTCCAAGTCTGACA	SAYSEDFENSPSLIASEPI
				GCATCTGAGCCAACCGCCCATTCCAAGGAGTCTCTTGACAGAACACTGGAC	AHSKESLDRTLDALSESSS
				GCTTTGTCTGAATCCTCTTCAAGTGTGAAGACAGACCTTCCACAAACAGCCG	SVKTDLPQTAESRKKSGRH
			_	AGTCTAGGAAAAAGTCGGGCAGGCACGTGACAAGAGTGCTTGTGAAGGACA	VTRVLVKDTAVQTPDPAFT
				CAGCTGTGCAGACGCCAGATCCTGCCTTCACCTACGAGTGGACCAAGGTGG	YEWTKVASMAAMGPALGG
				CCAGCATGGCAGCCATGGGGCCTGCCCTGGGAGGCGCCTACGTGGACCCG	AYVDPTPIANHVISADAIEAL
				ACACCCATCGCCAATCATGTTATCAGTGCAGATGCAATAGAAGCCCTGACCG	TAYSPAVLALHDVLKQQLS
				CTTACAGCCCGGCCGTGCTGGCACTCCATGATGTGCTGAAGCAGCAGCTGA	LTQQFIQASRHLHASLLRSL
				GCCTGACGCAGCAGTTCATCCAGGCCAGCCGGCACCTGCACGCCTCCCTC	DADSFHYHTLEEAKEYIRC
				TECECTCCCTGGACGCGGACTCCTTCCACTACCACACCCTGGAGGAAGCCA	HRPAPLTMEDALEEVNKEL
				AAGAGTACATTAGGTGCCACAGACCTGCCCCACTGACCATGGAGGATGCCC	*
			-	TGGAGGAGGTGAACAAGGAGCTGTGA	
rd	N	prey20143	25	ATGGCAGAGAGCCGCCAGGACCTGGAGGAGGAGTATGAGCCTCAG11CCTG 253	MAESHODLEEEYEPOFLAL
ospD1			_	CGGCTCCTAGAGAGAAGAAGCTGGGACCAAAGCTCTGCAGAGAACCCAG	LERKEAG I KALURI QAEIQ
				GCTGAGATCCAGGAAATGAAGGAGGCTCTGAGACCCCIGCAAGCAGAGGCC	EMKEALHPLOAEAHOLHLO
				CGGCAGCTCCGCCTGCAAACAGGAACCTGGAGGACCAGAICGCACIIGIG	NANLEUGIALVÄGKÄDEEV
				AGGCAAAAACGAGATGAAGAGGTGCAGCAGTACAGGGAACAGCTGGAGGAA	COYNECLEEMEEHUHULH
				ATGGAAGAACGCCAGAGGCAGTTAAGAAATGGGGTGCAACTCCAGCAACAG	NGVOLQQQKNKEMEQLRL
				AAGAACAAAGAGATGGAACAGCTAAGGCTCAGTCTTGCTGAAGAGCTCTCTA	SLAEELSTYKAMLLPKSLE
				CTTATAAGGCTATGCTACTACCCAAGAGCCTGGAACAGGCTGATGCTCCCAC	QADAPTSQAGGMETQSQG
				TTCTCAGGCAGGTGGAATGGAGACACAGTCTCAAGGGGCTGTTTAG	AV*
Shigella	2	prey1418	23	CTGGGTCATCCCAGATCCCGAAGAGGAACCAGAGCGCAAGCGAAAGAAGG 254	WVIPDPEEEPERKRKGPA PKMLGHELCRVCGDKASG
Indep					

PODFERS DIRECT

		256	257	TECTTGTGTGCAA 258 YYLLDVSVGN'-RYVVCNRH TTGCATTGTTTAA INDLFTLLHINDLEV*CLGNY TGCCATCHATTAKIXX TTGCATCATCHATTA YXXXXCTCATCATCATCATCATCATCATCATCATCATCATCATCA
ANGECTICCGGCTTCCACTACAACGTGCTCAGCTGCGAAGGGTGCAAGGGGCTTCTTCCAGCTGCAAGGGTGCAAGGGTGCAGGGGTGCAGGGGTGTGCAGGTGTGGGGCAGGGCAGGGCGAAGTTGCACAGGGGAAGTTGCGAAGGAAG	ATRANGATIGANCOACGETCCACCANCOACCTETTACANGCTGGACTCGGTCT [255] TCATTCGGAGGAACCCTTTGGCTGGTCTCATCANTCATCGACCCTGGAGGAACTA CCCATTGAACCTGGTGGTCTCCTGGTGGGCACCCTCCCCGCGGGGAACTA TTGCGTGGTGTGTGAACCGTGGTGACTTCGCCTGGGAACGTCTCT GGGGGGTAACGTGCTGACCTGGAACCTGGTAACTTGCCCGGGAACGTTGCT GGGGGGACCCCAGTACCTGGACCAGAACTTGCCTGGCTTGGTGCT GGGGGGACCCCAGTACCTGGACCAGAACTTGCCTTGC	GCTGGGGATCGCGCTGGCGCGGAGGGCTTCTGGCACTCAGAA ATCGACTTAAACCTCCAGAGAGTGAAATCTTGTGTGACACTTCGCACCTGCCA ATCGACTTAAACCTCCAGAGAATCAAATCTGTGAGACTTCCACACTGCCA CCTGATTAACGAATTGAGCTGGCTCTGAAGATATTGAACTTGCAGCTTTCCAACT GCCTGATTAACTTGAGGGATTCAAATTCCCAGGACTCCACAGCTTTCCA CCAGATAACCTTGAAGGAATTACTAATGATGGATCTAAAAGAAAACCAA GGGCACAGGGAATTAAAAATCAGTCGTGGGTTTGATTGGCCTCATTCAATCC AGACGGGGAATTAAGAATCAGTCGTGGGTTTGATTTGGCCTCATTCAATCC AGACGGCAATTAAGAATCAGTCGTGGGTTTGATTTGGCCTCATTCAATCC ACATGGCATTCAATAGAATCAGTCGTGGGTTTGATTTGGCCTCATTCAATCC	NINKINKINANINKINKINKINKINKINKINKINKINKINKINKINKINK	TACTATITACTGGATGTCTCAGTAGGCATAGITTAGAGATACGITGTGTGTGCAA (288 TAGACATATAAATGATTTGTTTACAATTACTCATATAAATGATTTGTTGTTTATATATA
41040004410000	46	25	99	57
	prey67642	prey67648	prey67266	prey67267
	5	8	e	က
	Shigella ospD1	Shigella ospD1	Shigella ospC1	Shigella ospC1

HODEWARD TOTALOW

			TUNGGCNTNGGNTNGGGNGCNTNTGTNTNGNCNNNGTTGTTGNGNNNANG GCGNGNNCGRAINCNGTTGATTNNCAGGTNTGGNNNNGNTGGNGGCNCNT GGCNCCTNGCATNTN	XXVVXXXAXXXVDXQVW XXWXXXAPXX
Shigala 3 osp01	prey50590	88	GETTIGATGAGGGAGTTGAGGATTGAGTTGAGGGGGGGGGG	GONGETHALITHOLAK GUNKETTVIMDTCERONG KANEPGTIVOHOHYGGS GGRGSINSPCAVGRAGO GGRGSINSPCAVGRAGO GTOKANPYARATITENO GTOKANPYARATITENO GTOKANPYARATITENO GTOKANTITENO VTIPPGTOTDOKIRMGGKGI PRINSYG SODYHIKIRAP KRLTSRGOSILLSYAEDETD KRLTSRGOSILLSYAEDETD KGTVNOVTITESGGSTM DSSAGSKARFAGEDEG FLSKLKKMFTS*
Shigella 3 ospC1	prey9822	9	ATGGGGGACCTTGATTGGCGTCCGAAACTGTGAGGGGGTGGAGGGGCCGTCT 280 AGGGGGTGGGGGGTGGCGCTGCTGAAACTCTCCGCTGAGCTCATTCG GAGGGGGGGGGG	MADLDSPRAGNOOPSE GWGGGACSEISALIBSITE LOELEAVYER.CGEEKVVE HENDALLEGOANIESKIMTL HENDALLEGOANIESKIMTL HENGENLOLIEGDAKOLG MITTONLAENVSSKYRQL DLAKNET,CANGARDDILDI KFOMOGVOTALRSEDYGO KFOMOGVOTALRSEDYGO AAAHHRYTCLDKSVIESBY GOKGGSMIDANICLOFEGE RAFSEYLCKOVASKAEINL LIVILEGGARIUSKIPTEGOL TYYGPGSMIDANICHOPIVE TYYGPGRATTLIKTOVEG TYYGPGRATTLIKTOVEG TYYGPGRATTLIKTOVEG TYYGPGRATTLIKTOVEG TYYGPGRATTLIKTOVEG GPRHYGNNINGNITEKIE PRELIDPILTEVILUMARSEL

IDOHENST DIFFIE

				TACCACCAGCAGTTCCGGCATGTTCAGAACAACCTGATGAGAAATTCTACAA CAGAAAAATCACAACCAAGAACTGGACCCAACTCTGAGTGAG	YLAFLKKAISSDFEVGDSM ASEEVKORLOKLINN CLISCTMOELIGYTWIEG CLISCTMOELIGYTWIEG CLITSSMADDVETVYKKGGA ALSSSIDCLCAMINLATTE ELESPERVLCKIKLENGFPA TTFODIORGYTSAVIMMS TTFODIORGYTSAVIMMS TTFODIORGYTSAVIMMS KKTLESDCTKLESOGIGGE GAGAKFDGGLSDLAVSNK HBULGGGTTELNSTAKPO NOPWINSTENSYSHINEEEF
				AAGTITGAGGGCTGCCTTCTGACTTGGCGCGGCGTCTCCAACAATTCCGAG ACCTCTTGCAGGAAGGGCTGAGGGGGCTCAACAGGCATCAAGGCGA GGGAGAGGCGTGAGGGGGGTGTCAACAGCATCAACAGCTTCCAACAACATCACAGGGGGGGG	OMAEKASENYUSUSTGI. MTSI.VAVELEKVU.KSTFN RLGGLOFDKELRSLIANLTT VTWTTBOKZAR.SOMATIL NLEHYTELDYWGPNSGPL TWRLTPAEVROVLALRIDF RSEDIKRLRL*
Shigella ospC1	ო	prey67268	09	COGNICT GEOTIGE CONTINUE AND ASSET OF THE STOTITION OF THE SECTION	PCLGWLIYQGCLSLCL'LGY FTT'-R*KFVSALILM'IIPV HKTANYIECN'LWPCRHSR VLPVCTHL'MGFSISYLTINV LLLIYTNHLS
Shigella ospC1	ေ	prey67270	19	NONGGTGNGTGNGTGNGTGNGAGTNINANCTNTGCGACTGCATGNTGTTTTGGTC 282 AGGCNIGATNINATGNGTGTTCACTTTTATGAGGTTCCANNATTCAAATGGATN TGATGGATAACTTCCCCATGACTTTATTGAAGTTCATGAGGGTGGNN TNNCTNNTNNTCTATNGATCATTAGATNINNINNNCACTGTTGNGGGTTGGNN TNNCTNNTNNTCTATNGATCATTAGATNINNINNNNCACTGTTGNATGATCCATTAGATNINNINNNNCACTGTTGNATGATCGTTCATAGATNINNNNNNCACTGTTGNATGATCGTCTTCATAGATTCATAGATNATGATCGTCATTGAATGATCGTCATTAGATCGTCTCATAGATCGTCTCATAGATCGTCTCATAGATCGTCTCATAGATCGTCTCATAGATCGTCATTAGATCGTCTCATAGATCGTCATAGATCGTCATAGATCGTCATAGATCGTCATAGATCATAGATCGTCATAGATAG	XGXXRXSXXPLHXVLLRX DXC1FMKFXXSNGXDA* PSPCXXCTGSAGLXLXXL XXIRXXXTLXLSXLSGP* XICXSHX*SXXXXPXIS

ADDITION OF PARTY

				COULTITIONAL CONTROL C	A LIBOURGIONORIUM
Shigella	က	prey67271	62		ZELGNINGERGYGEDGI LEN
lospC1				ACT GAAGAT CAAGC GGGGCAC AT GCCACACAGC CCAGAAACACACACACAAAAAAAAAA	EI VBCIBHII VNEOBI VBEA
				CCGCI GCCCCAI GGAGCI GGI CCGCCAI CCGCCAI AI 191 ACAA 1 GAA	TEACH INCIDENTED
				CAGAGGTTGGTCCGAGAAGCCAACAAIGGIAGCICICCAGCIGGAAGCCII	NGSSPAGSLADAMSCRA
				GCTGATGCCATGTCCCAGAAACACCTCCAGATCAACCAGACGTTTGAGGAG	COINOT FEEL RLV I QD I ENE
			_	CTGCGACTGGTCACGCAGGACACAGAGAATGAGTTAAAAAAGCTGCAGCAG	-KKLQQTQEYFIIQYQESLR
				ACTCAGGAGTACTTCATCATCCAGTACCAGGAGAGCCTGAGGATCCAAGCTC	QAQFGPLAQLSPQERLSR
				AGTTTGGCCCGCTGGCCCAGCTGAGCCCCAGGAGCGTCTGAGCCGGGAG	ETALQQKQVSLEAWLQRE
			_	ACGGCCCTCCAGCAGAAGCAGGTGTCTCTGGAGGCCTGGTTGCAGCGTGA	AQTLQQYRVELPEKHQKTL
				GGCACAGAGACTGCAGCAGTACCGCGTGGAGCTGCCCGAGAAGCACCAGA	ALLRKQQTIILDDELIQWKR
				AGACCCTGCAGCTGCGGAAGCAGCAGCATCATCCTGGATGACGAGC	RQQLAGNGGPPEGSLDVL
				TGATCCAGTGGAAGCGGCGGCAGCAGCTGGCCGGGAACGGCGGGCCCCC	QSWCEKLAEIIWQNRQQIR
				CGAGGGCAGCCTGGACGTGCTACAGTCCTGGTGAGAAGTTGGCGGAGAT	RAEHLCQQLPIPGPVEEML
				CATCTGGCAGAACCGGCAGCAGATCCGCAGGGCTGAGCACCTCTGCCAGCA	AEVNATITDIISALVTSTFIIE
				GCTGCCCATCCCGGCCCAGTGGAGGAGATGCTGGCCGAGGTCAACGCCA	KQPPQVLKTQTKFAATVRL
				CCATCACGGACATTATCTCAGCCCTGGTGACCAGCACGTTCATCATTGAGAA	-VGGKLNVHMNPPQVKATII
				GCAGCCTCAGGTCCTGAAGACCCAGACCAAGTTTGCAGCCACTGTGCG	SEQQAKSLLKNENTRNDYS
				CCTGCTGGTGGGGGGAAGCTGAACGTGCACATGAACCCCCCCC	GEILNNCCVMEYHQATGTL
				AGGCCACCATCATCAGTGAGCAGCAGGCCAAGTCTCTGCTCAAGAACGAGA	SAHFRNMSLKRIKRSDRRG
			_	ACACCGCAATGATTACAGTGGCGAGATCTTGAACAACTGCTGCGTCATGGA	AESVTEEKFTILFESQFSVG
				GTACCACCAAGCCACAGGCACCCTTAGTGCCCACTTCAGGAATATGTCCCTG	GNELVFQVKTLSLPVVVIVH
	_			AAACGAATTAAGAGGTCAGACCGTCGTGGGGCAGAGTCGGTGACAGAAGAA	GSQDNNATATVLWDNAFA
			_	AAATTTACAATCCTGTTTGAATCCCAGTTCAGTGTTGGTGGAAATGAGCTGGT	EPGRVPFAVPDKVLWPQL
				TTTTCAAGTCAAGACCCTGTCCCTGCCAGTGGTGGTGATCGTTCATGGCAGC	CEALNMKFKAEVQSNRGLT
				CAGGACAACAATGCGACGGCCACTGTTCTCGGGACAATGCTTTTGCAGAG	KENLVFLAQKLFNNSSSHL
				CCTGGCAGGGTGCCATTTGCCGTGCCTGACAAAGTGCTGTGGCCACAGCTG	EDYSGLSVSWSQFNRENL
			_	TGTGAGGCGCTCAACATGAAATTCAAGGCCGAAGTGCAGAGCAACCGGGGC	PGRNYTFWQWFDGVMEVL
				CTGACCAAGGAGAACCTCGTGTTCCTGGCGCAGAAACTGTTCAACAACAGCA	KKHLKPHWNDGAILGFVNK
				GCAGCCACCTGGAGGACTACAGTGGCCTGTCTGTGTCCTGGTCCCAGTTCA	QQAHDLLINKPDGTFLLRFS
				ACAGGGAGATTTACCAGGACGGAATTACACTTTCTGGCAATGGTTTGACGG	DSEIGGITIAWKFDSQERMF
				TGTGATGGAAGTGTTAAAAAAACATCTCAAAGCCTCATTGGAATGATGGGGCC	WNLMPFTTRDFSIRSLADR
				ATTTTGGGGTTTGTAAACAAGCAACAGGCCCATGACCTACTGATTAACAAGC	LGDLNYLIYVFPDRPKDEVY
				CAGATGGGACCTTCCTCGTGAGATTCAGTGACTCAGAAATTGGCGGCATCAC	SKYYTPVPCESATAKAVDG
			_	CATTGCTTGGAAGTTTGATTCTCAGGAAAGAATGTTTTGGAATCTGATGCCTT	YVKPQIKQVVPEFVNASAD
				TTACCACCAGAGACTTCTCCATCAGGTCCCTAGCCGACCGCTTGGGAGACTT	AGGGSATYMDQAPSPAVC
			_	GAATTACCTTATCTACGTGTTTCCTGATCGGCCAAAAGATGAAGTATACTCCA	PQAHYNMYPQNPDSVLDT
				AATACTACACACCAGTTCCCTGCGAGTCTGCTACTGCTAAAGCTGTTGATGG	DGDFDLEDTMDVARRVEE
				ATACGTGAAGCCACAGATCAAGCAAGTGGTCCCTGAGTTTGTGAACGCATCT	LLGRPMDSQWIPHAQS:
				GCAGATGCCGGGGGGGCGCCACGTACATGGACCAGGCCCCTCCCC	

TOOTSTRY GILLOR

				AGCTGTGTGTCCCAGGCTCACTATAACATGTACCCACAGAACCCTGACTCA GTCCTTGACACCGATGGGGACTTCGATCTGGAGGACACAATGGACGTAGCG CGGCGTGTGAGGAGGAGACTCTGGGCCGGCCAATGGACAGTCAGT		
		prey/700	88	ATGGGAATTGGTCTTCTGGTCAAGGTTGAACATGAATAGACAACAGGGTT CGGGGAAACTGGACAAGGTTGAACAATGGAATACAGAATTGGTTTGTT TCTGGAAACTGGACAACCTATGGTTACATACTGGTTGTTTGT	MAGIGLSGONWINNIPPOW MAGIGLSGONWINNIPPOW MALINITICATTAGOLFSCIS VALINITICATAGOLFSCIS VALINITICATAGOLFSCIS VADANGOLFPORDEDY REWATKIOAQIDAFPIGDE REGNOTMICKANSSYLVH HGYCATAGARAARSTOATA EELSKINNIPPOLISIUS HGYCATAGARAARSTOATA EELSKINNIPPOLISIUS MAGAETUCOL YPSLIERN PALLETLAYROFIEMWOT DSEVRCLGGRSPKSODSY POSPRASSENSKISHEN NEWSPKSODSY NAGOSTOATAGOLF NAGOSTOATA	MMNRHPGW MMNRHPGW (NGHSLGIA (NGHSLGIA (NGHSLGIA MNSSYLVH RSTDOTYL OKLVLAGE MSSYLVH RSTDOTYL OKLVLAGE MSSYLVH RSTDOTYL OKLVLAGE MSSYLVH MSSYLVH MSSYLVH MSSYLVH MSSYLVH MSSYLVH MSSYLW MS
Shigella ospC1	en en	prey3486	49	GATCGAGATCATCATGGAGATGATCATCATCATTGATGATGAGAGAGA	GENGARAGE CESCHILL CELL GRAVIOSE GENERAL SOCIETATO SOKEGYNLTAVEGTIGDFK AYALAGVSFEIKAEDDOPL PGVLLSLSGGLFRSNLTO	SPLITVFTD HSDLEYTVT FEGTIGDFK (AEDDQPL FRSNLLTQ

TOCKETS/ OLITICE

			SOM NO SECTION OF THE CONTINUE OF THE CANADA	INGII TESNI SPGOVYEKP
			TTATCCCTGAGCGG GGCCTGTTTCCAAACCTCTGGCCAGTTTTCAAACCGAT	MMKEFRFEPSSOMIEVOE
			GATGAAGGAGTTTCCGGTTTTGAGGCGTTCCGCGAACCGGCTTACAGTTG	VSSLNGEPEQGVAMEAVG
			CTATGGCACAGTGTCTTCCTTAAACGGAGGCCCGAACAAGGGGGTTGCCAT	QNDCSIYGEDTVTDEEGKF
			GGAAGCGGTGGGCCAGAACGACTGCAGCATTTACGGAGAAGACACCG GAC ACACCAACGAGGGCAACTTCAGATTACGTGGATTGCTGCCGGGATGTGTGTA	NDHIERALPHHRVIEVGNN
			CCACGTTCAGCTCAAGGCAGAAGGCAACGACCACATTGAGCGGGCGCTCCC	DIDDVNIIVFRQINQFDLSG
			CCACCATAGGGTGATTGAGGTTGGGAATAATGACATCGATGATGTAAACATC	NVITSSEYLPTLWVKLYKSE
-			ATAGITITICCGGCAGATTAATCAATTTGATTTAAGTGGAAATGTGATCACTTC	NLDNPIGI VSLGGSLFFHFF
			CTCTGAATACCTTCCTACATTATGGGTCAAGCIIIACAAAAGCGAAAACCICG	SOYDYII POVSETAVGYHK
			ACAA LOCAAT COAGACGGGGGGAGAACTATGTTGTGCTTCTGGACTCCACACTCC	HTTLIFNPTRKLPEQDIAGG
			CCAGATCCCAGTATGACTACATCTTGCCTCAAGTTTCTTTC	SYIALPLTLLVLLAGYNHDK
			CTACCATAAACACACCACCTTGATTTTTAATCCCACGAGGAAGCTGCCTGAA	LIPLLLQLTSRLQGVRALGQ
			CAGGACATCGCACAAGGATCCTACATTGCCCTGCCATTGACGCTGCTGGTTC	AASDNSGPEDAKHQAKKQ
			TGCTGGCCGGTTACAACCATGACAAGCTCATICCTIIGCIGCIGCAGIIGAC	ואוע
			AAGCCGGCTACAGGGAGTCCGCGCTCGGCCAGGCAGCCTCTGACAATA	
			GCGGCCCAGAAGATGCAAAGAGACAAGCCAAGAAACAGAAGACAAGACGGA	
Shinella 3	prev14801	65	CCTGGGCCTACATTCTCCCATTGCCCTAGATGTACTGAGTGAG	LGLHSPIALDVLSEAFEESL
			GAATCCTTGGTGGCCAGAGATTGGTCCCGGGCCCTTCAGCTCACTGAAGTG	VARDWSHALQLIEVYGHD
			TACGGGCGAGATGTGGACGATTTGAGCAGCATAAAGGATGCAGTCCTGAGC	VDDLSSIKDAVLSCAVAYD
			TGTGCTGTGGCATATGACAAAGAAGGTTGGCAATACCTGTTTCCCGTGAAGG	KEGWQYLFPVKDASLHSHL
			ATGCATCTCTGAGAAGTCGGCTGGCCCTACAGTTTGTGGACAGGTGGCCCC	ALQFVDHWPLESCLEILAY
			TGGAGTCATGCCTGGAGATTCTGGCCTACTGCATTTCAGACACGGCTGTCCA	CISDTAVGEGLKCELGRKL
			AGAAGGACTAAAGTGTGAGCTACAGAGGAAGCTGGCGGAGCTGCAGGTGTA	AELQVYQKILGLQSPPVWC
			TCAGAAGATTCTGGGTTTGCAGTCTCCCCCAGTGTGGTGTGACTGGCAGAC	DWOTLESCCVEDPS I VMN
	_		CTTGAGGAGCTGTTGTGTTGAGGACCCATCAACTGTCATGAACATGATTCTA	MILEAGEYELCEEWGCLYP
			GAAGCACAGGAGTATGAACTGTGTGAAGAGTGGGGGCTGCCTGTACCCCATT	IPREHLISCHORHLCHCLER
			CCAAGAGAACATTTAATCAGCCTTCATCAAAAGCATCTTCTCCACCTTCTAGA	RUHUNALQLLHHIPUPI INC
			AAGAAGAGATCATGACAAGGCTCTGCAACTCCTGCGAAGAATCCCTGACCCC	LEVTEQSLDQHTSLATSHF
			ACCATGTGCCTTGAAGTGACAGAGCAATCCCTCGACCAGCACACTAGCT1GG	CANYLI HEYGOLI AVRHR
			CCACTTCTCACTTCTTGGCCAACTACCTCCACCCACTTCTTTTTTTT	A SYSTEM SOND ENTERIN
			ACTGCTGTCCGACACCGTGAAAICCAGGCGCIGIAIGIGGGAICCAAGAIIC	NAKYOWATVAVOTI OOLI
			TGCTGACCCI GCCI GAGCAGCAGCAGCAGCI AL I CCCACI I GI CCI CI AN	VGOEIGETMDEVDSI JSBY
		_	CCCCCIGII CAI GCI GGAGCAGCI GCI I AI GAACAI GAAGGI GCAI I CCCC	A EKAI DEPYPOBEKBSDSV
			CACTGT GGCT GT GCAGACT CT CCAGCAGCT GCT GGT T GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	IHLOEIVHQAADPETLPRSP
			CITCACIAI GGACGAGGI GGACI CACI I CONCALI CONCALI CACI	5

ICC+W+W> DIFFIC

LEAFKRIPPQELEGLIQAIHN OILOPAAVTRLRNQLLEAEY WHAWGMACLKAGNLTAAR **CEMKDOVBAAMTCIBFESH** TFFRKKMTAADVSRHMNTL DVACKVMLGGKNVEDGFGI **AFRVLQDFQLDAAMTYCRA** EKFSRCLKPPFDLNQLNHG TOSLSLAVIPEGKIMNNTYY VSESGMAAKSDGDTILLNC **DDNKVRAYLICCKLRSAYLI** AVKQEHSRATALVQQVQQ SRLVQDVVEYLESTVRPFV PEVFIEGIFQPSYKSGKLHT KAKSYTELGEKLSWLLKAK RERSEPPTOPSOEFVPPAT CCBEHFTMFNBBHHCBBC DLKEEENELVRSEFYYEQA DAGLLTDIMKQLLFSAKMM SLQDDDYFATLRELEATLR LENLLESIDPTLESWGKYLI AACQHLQKKNYYHILYELQ SQITTLPLPTLFGNNHMKM ARQLVEKEKYSEIQQLLKC SAEFSPAAPPGISSIHSPSL **PPARHQWVPDETESICMV** GRLVCSSCSTKKMVVEGC RENPARVCDQCYSYCNKD VPEEPSEKPEALDSSKSES PPYSFVVRVPKADEVEWIL HOLIEHCCRLSKGLTNPEV FVKAGQSQDLALCDSYISK VDVLNILVAAAYRHVPSLD QECLFYLHNYSTNLAIISFY VRHSCLREALLHLLNKESP DHLKIYLQETSRSSGRKKT QLQMEVTRFLHRCESAGT **PSASLCIAILNLHRDSIACG** YOLGVEVSTKTGLDTTGA GTCATATACAGAACTGGGAGAGAAGCTCTCATGGCTACTTAAGGCCAAGGAC CACAAAGACTGGGCTTGATACCACCGGGGCGTGGCATGCTTGGGGCATGGC CAGGATGTGGTTGAGTACCTAGAGTCCACAGTGAGGCCCTTTGTATCCTTGC AAGATGACGATTACTTTGCCACCCTGAGGGAACTGGAAGCTACCCTTCGGAC TCATCAGCTTCTACGTGAGGCACAGCTGCCTGCGGGAAGCTCTTCTGCACCT CACACTTCAGCTGCAGATGGAAGTGACCAGGTTCTTGCATCGGTGCGAAAGT ATCAGCAGAGTTCTCTCCTGCTGCTCCTGGTATCTCCAGTATACATTCCC AGAGTATCTGCATGGTCTGCTGCAGGGAGCACTTCACCATGTTTAACAGGCG CCTTGTGCATTGCCATCCTGAATCTGCACCGGGACAGCATTGCCTGTGGTCA GGTGGATGCCGGGCTGCTCACGGACATCATGAAGCAGCTGCTGTTCAGCGC CAAGATGATGTTCGTCAAAGCCGGCCAGAGCCAAGACTTGGCTCTTTGTGAC GCCACGTGCCATCTTTGGATCAGATCTTGCAGCCAGCTGCAGTAACCAGGCT TCTGAAGCCCCCATTTGACCTCAATCAGCTGAATCATGGCTCAAGGCTGGTG GCAGAGCCTTTCTCTGGCAGTGATTCCTGAAGGGAAAATCATGAACAACACC ACCAAGTTCGGGCCGCCATGACCTGTATTCGGTTCTTCAGTCACAAAGCAAA CCACATTCTTCAGAAAGAAGATGACTGCAGCTGATGTGTCAAGGCACATGAA GCTGGGACCTCTCAAATCACCACTTTGCCTCTGCCAACCCTGTTTGGAAATA AGAAGATGGTTTTGGAATTGCTTTCCGTGTTCTGCAGGACTTCCAGCTGGAT GAAGCTCTAGACAGCTCCAAGAGTGAAAGCCCTCCATACTCGTTTGTGGTGA CTGCCTCAAAGCCGGGAACCTCACTGCTGCACGGGAGAAGTTCAGTCGCTG TACTACCAGGAATGCCTCTTCTACCTGCACAACTATAGCACCAACCTGGCCA GCTATAAAAGTGGGAAGCTACACACTTTGGAGAACTTGCTAGAATCCATTGA CAGAAGAAGAACTACTACCACATTCTGTATGAGCTGCAGCAGTTTATGAAGG CTGGACTTTCCATACCCTCAGAGGGAGAAACGATCAGATTCTGTGATTCACC CTAGTCTAAGGGAAAGGAGTTTCCCACCAACCCAGCCCTCACAGGAATTTGT GTGCTATAGTTACTGCAACAAAGATGTACCAGAGGAGCCTTCAGAAAAACCA GAGTCCCCAAAGCAGATGAGGTGGAATGGATTTTGGATCTCAAAGAGGAGG CCAGCTGATTGAGCACTGCTGCAGGCTCTCCAAGGGCCTCACCAACCCAGA AGCTACATCAGCAAGGTAGATGTGCTGAATATTTTAGTTGCTGCTGCTATC AAGGAACCAGCTTTTGGAAGCCGAGTACTACCAACTGGGCGTTGAGGTCTC GCCCCAGCGACACCCCTGCCAGGCACCAGTGGGTACCGGATGAGACTG TCATCATTGTCGCCGCTGTGGCCGGCTAGTGTGCAGCTCCTGCTCCACTAA AAAATGAGCTGGTGCGGAGTGAATTTTACTATGAGCAGGCCCCCAGCGCCT

CONTRACTOR OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY OF

			ACCTACTECAGAGCTGCCCGCCAGTTGGTGGAGAAAGAGAAGAG	AAKSSGDAVVQDICAQWLL TSHPRGAHGPGSRK*
Shigella 3 ospC1	prey67279	99	267	LPLCIAGEL*IIICVIAYSFLNI FTFIISFNFHTSPEKCFFHFT YYDAEAQQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Shigella 3 ospC1	prey67280	29	568	NFHLPREVYVEF*ALFYVFT SLSHTATRIHTHSLFLIK*DY TTHILSJAFLLKSISKRILCVS TGAGTSFF*LAAWRSIEGLS SCV*PSGWIVCLFLVX
Shigele aspC1	prey49194	89	COCCOCTOGGGAAGGA GGGGGGAGGGTCGACAT COGGCGGAGGGTCCACAT SOCCOTTOTAACAGGTGC AAGGGGGTCGTCATCA SOCCOTTCATCTCTCACA COCTCCTCGTGTTCAAT TOATCACAGGTTGAAT TOATCACAGGTGGTGC TTCATCACAGGTGGTGC TTCATCACAGGTGGTGC TTCATCACAGGTGGTGC TTCATCACAGGTGGTGC TTCATCACAGGTGGTGC TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTCCAGGTG TTGCTGACATTGCCCATTCCC CCCCCCACTTGCCCATTCCCC CCCCCCCACTTGCCCCATTCCCC CCCCCCCACTTGCCCCCCCCCC	INPOPELVABLESPADSBRIH WASGYCOLEGGDAFALEK SI SOHYGRBSWHEVLCTL GOSKTLEFNKCSLLNAHAD HKSKGLWOGGSQLTKRIB ADOMIN-VSAPANYNSTRAAPA ADOMIN-VSAPANYNSTRAAPA ALPLYPDPVILIRYSIKCLE CHKOMROWNALAHORT TEFTEGLTCOVCANLLNO CHKOMROWNALAHORT TETTEGLTCOVCANLLNO CLHVARKVGYRCHGGWH CLHVARKVGYRCHGGWH CAFCPMAFKTASSTADHSA CAFCPMAFKTASSTADHSA CAFCPMAFKTASSTADHSA CAFCRAHOGHFSQLIVKGSC EMYFRIKGHIGGHFYQWY KTOMINGKHIGGHFYQWY CAFCRAHOGHFYGWY CAFCRAHOGHFYGWY CAFCRAHOGHFYGWY CAFCRAHOGHFYGWY CAFCRAHOGHFYGWY KTOWIGWYRCGECPLLFYQK KTOWIGWYRCGECPLFYQK KTOWIGWYRCGECPLFYQK

TOOTEHOY DELLON

				TO A SALES
			CAACAAGAAGAGGCACATTCAGCAGCATTTTTACCAGAATGTCAGCAAGACG	PELMOHVKSTHGVPRNVD
			CAGGTGGGCGTCTTCAAGTGCCCTGAGTGCCCACICIIGIICGIIGCAGAAG	ELSINEGSSADI SSSRFGSR
			CCGGAGTTGATGCAACACGTCAAGAGCACCCACGGTGTTCCCCGAAA1G1G	VPI EPPAI SVAAHSSSLPS
			GACGAGCTGTCAAACCTCCAGTCTTCAGCGGACACATCCTCAAGCCGCCCT	GRWGRPEAHRHVEAHPHL
			GGCTCTCGAGTTCCCACTGAGCCACCAGCCACTAGTGTGGCTGCTCGGAGC	RNTGWTCQECQEWVPDR
			AGCTCCCTGCCTTCTGGCCGCTGGGGTAGGCCTGAAGCCCACCGCAGGGT	ESYVSHMKKSHGRTLKRY
			GGAAGCCAGGCCGCGGCTGAGGAACACTGGCTGGACCTGCCAGGAGTGCC	PCRQCEQSFHTPNSLRKHI
			AGGAGTGGGTTCCAGATCGGGAGAGCTACGTGTCCCACATGAAAAAGAGCC	RNNHDTVKKFYTCGYCTE
			ACGGTCGGACATTGAAGCGGTACCCATGCCGGCAGTGTGAACAGTCCTTCC	DSPSFPRPSLLESHISLMH
			ACACCCCAACAGGCCTGCGCAAACACATCCGCAACAACAACAACAAAAAAAA	GIRNPDLSQTSKVKPPGGH
			GAAGTTCTACACCTGCGGGTACTGCACAGAGGACAGCCCCAGCTTTCCTCG	SPQVNHLKRPVSGVGDAP
			GCCTCCCTTCTGGAGAGCCACATCAGCCTTATGCATGGCATCAGAAACCCT	GTSNGATVSSTKRHKSLFQ
			GATTTGAGCCAGACGTCCAAAGTGAAACCTCCGGGTGGACATTCCCCTCAG	CAKCSFATDSGLEFQSHIP
			GTGAACCATCTGAAAAGACCAGTCAGTGGAGTGGGGGACGCTCCAGGCACC	QHQVDSSTAQCLLCGLCYT
		_	AGCAATGGCGCAACTGTCTCTTCCACCAAAAGGCACAAGTCCCTTTTTCAGT	SASSLSRHLFIVHKVRDQE
			GCGCGAAATGTAGTTTTGCCACAGACTCGGGGCTCGAGTTTCAGAGCCACA	EEEEEEAAAEMAVEVAEP
			TACCTCAGCACCAGGTGGACAGCTCCACAGGCCCAATGTCTCCTCTGTGGTTT	EEGSGEEVPMETRENGLE
			GTGCTACACCTCTGCCAGCTCCCTCAGCCGCCACCTCTTCATTGTCCACAAG	ECAGEPLSADPEARRLLGP
	_	_	GTGAGAGACCAGGAGGAGGAGGAGGAAGAGGAGGAGGCGGCG	APEDDGGHNDHSQPQASQ
			TGGCAGTGGAGGTGGCAGAGCCAGAGGAGGGCTCCGGGGAGGAGGAGGTGCC	DQDSHTLSPQV*
			CATGGAGACTAGAGAATGGACTGGAAGAATGTGCCGGTGAGCCTTTGTC	
			AGCTGACCCAGAGGCGAGGAGATTGCTGGGCCCGGCCCCTGAGGACGATG	
			GTGGCCACAATGATCACAGTCAACCACAGGCCTCTCAGGACCAGGACAGCC	
		_	ACACACTGTCCCCTCAGGTGTGA	
Shinella 3	prev67287	69	GAACACTCCTCTAGCTTATGCTGTTCTTTTAAGTTTGTCTTTGAGTTGG 270	EHSSSLVMLFF*VCL*VGKV
			GAAAGTAGACCTATTTGGCTTGGCTTAAGGGCTAAATGTCTCCTCTTCACTTG	DLFGLA*GLNVSSSLGLLILS
			GTCTTCTAATCCTCAGTCCTTCCTGGCTATGTGGCATCATGTCTTTAAAGCAG	PSWLCGIMSLKQGE*SINIL
			GGAGAGTAAAGTATCAATATTTTAAGAAGGAACATTCTTCCCACTTACGTTTT	RRNILPTYVFYSSFF*ALSR
			CTATTCTTCTTTTTGAGCCCTTTCTAGAAAGAGTAATGCTCTAGCCTTCAA	KSNALAFNQK*KVY
		i	CCAGAAAIGAAAAGICIAIG	VHOVTDI SBNAOI EKBSI I
Shigella 3	prey19931	2	GGTGCACCAAGIGACAGACCIIICIAGAAAIGCCCAGCIGIICAAGCGCIGI	EMATE*
	00020	7	FIGURGAGGGGATGGGGAGGTTATAACNNNATNTTCTTTTGGTANTNATA 272	GGVGMGR**XXXLLVXIQC
Strigeria 3	než roće id	_		GXLX*XXLXTXNIFFXSYLS
oden			NTOTTATCTTTCTNTTGTCTTCTGTGGGAGANGGCTGCTNTNTTTTTANNGN	XVFCGRXLLXFLXXLXIFXIS
			NI CHARLES AND	RISAXI XLXYFMXXXLXXXX
			TTTATE ANATANNITE CITATA AN CONTRA AND A TOTAL AND A TATA TATAL AND A TATAL A TATAL AND A TATAL A TATAL AND A TATA	NLINIYXLXLHHIXXIF
			NATITACATCATATAGANNATATCTTT	
Shinella	nrav67291	72	TTTGAAGGGNTCNTANNAACATAGGANAATGTGGCTATAGTTTGGAACCTNC 273	FEGXXXT*XNVAIVWNLLHI
		1		

ACIHAMBY DIIIDE

				ACRONGEDOWKETVOTOTO ACROSTIC SERVENTONY NETECARK SRWENDOWNT NETECARSCEGENWSKAR GSRFSVAEHGEPYKECO REPLOANKLSSTEVLSTOT DSSSAEDSDFEEMGKNIE MICHARLAAGSAASG NNHRDDTASYTSTEVLSSTOT ROETVRYTFRDEGKEYV ROETVRYKRANDAVNRHTT KOEETNRKAALFOEGHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE MRKERHRIGGCHREE ROEKKLKOPPEKKRKMKE REDKLKCOACGAIGHRET
TACATATTIGITGAATGGCITTGACANACTTGCTGATAGTGATATGAACATTA NNGTCCAAGCTGAGGTGCTCCAAATGGAGAGTGAGGAACTTGTTGGGAACT GAGGAGACGAGAGAGAGCAGTGTTTGGACTTTTGCAGTTTTAGAGAGACCAGTGTTTGACCACTGTTTGCACTTTTGCACTATTGAGANAATTTGAGAACTTTAGAGAACTATAACATTGAGANAANATTGAGAACTTTAANACNTTGAGANAANATTAATAANACATTAANACATTAANACATTAANAATAAACATTAANAAATAAAAAAAA	GCACAAGCCGTCATACCATACCAGGCAGTAAAATTTACTCCTTAGTTTCTTCTT CTANAAATTAGATTAGTCTGTGATCCATTTGGGTTAATTTTTCTGTGATGTATTTTCT ACATTGATTGATGATTATTTTTTTCTAGTTTTAAAATTTTCATCAGTTGTTCA ACCHTCATTGATTGAGAAAATTGTTNTCCCATAANATTATTCATGCAGTTGTCA NGNGTGAGNANNINTATTAGGGGCTTAANAATTGANAATAGCT NGNGTGAGNANNINTATGAGAANAACTGTNGGGTGGG	AGAGTGGGGATGGGCTGGGCCTCTGTCGTCCGTCCGACCCCCCTCATGTG 275 TGCTGCCCCAAGCTCGCCGCTCCCTAGTTGGTATTCTGTGCGGCCTGG GGTATGGTGGAACCCGCCGCTCCCTAGTTTGGTATTCTGTGCGGCCTGG GGTATGGTGGAACCCAGACTCAATCTTGGGCTCCAGTTTCG CCTCCTGGGGTCTGCTCGGGGTCGGCGTCAGTAATTAACCCGGGTCCCAAGGGTTG TCGTCTTCCCCCCAGGGGTGGGGCGCTGCCTGTACATGCCAGGGTTTT GCAGGCTTTTCATCCANATTTGTTCATCATTAACCTGTACATGCCAGGGATCTTTT GCAGGCCTTTTCATCCANATTTGTTCATCATTAACCTGTACATGCCAGGGATCTTTT GCAGGCCTTTTCATCCANATTTGTTCATCAATGCCAGGGATCTTTT CCACCAAGACTCAACAACAACAACAACAACAACAACAACAACAACAAC	CCTCCTCCTCCAACACGTGGACACAGTGTCTGCCCAATGCTACTTTTTTTT	AGCAGAAGGATGATAAGAACGCAGCAGCAGAGAGAGAGAG
	73	74	22	76
	prey67294	prey67296	prey67299	prey4637
	e e	ю.	ю	ю
ospC1	Shigella ospC1	Shigella ospC1	Shigella ospC1	Shigella cspC1

IDOKSABY DILIBE

				17000	A VOINDOON INTO CONTINUE
				_AAGCCCAAGAAAATGAAGGAGCGTCCTGACCTAAAACTGAAATG1GGGGCA1	NATCELY TO INAPPOINT VA
				GTGGTGCCATTGGACACATGAGGACTAACAAATTCTGCCCCCTCTATTATCA	MTEEQEEELEKI VIHNUNE
				AACAAATGCGCCACCTTCCAACCCTGTTGCCATGACAGAAGAACAGGAGGA	ELIKVEGTKIVLGKQLIESAD
				CONSTRUCTION AND ACTOR TO THE AT GAT AND A TO THE ACT TATCA BE GETTED.	EVRRKSLVLKFPKQQLPPK
				GOOD ON THE TOTAL OF THE TOTAL	KKRRVGTTVHCDYLNRPH
				A A CONTRACT TO THE CONTRACT T	KSIHBBBTDPMVTI SSILESI
				CGCAGAGAAA CTCGGGT CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	INDMEDI PNITVPEHTBVNA
				AAGAAACGGCGAGIIGGAACCACIGIICACIGIGACIAIIIGAAIAGACCO	KAAKOVKITEBANI OTI B
				ATAAGTCCATCCACCGGCGCGCACAGACCCIAIGGIGACGCIGICGICA	NAVA INITIALIZATION
				TCTTGGAGTCTATCATCAATGACATGAGAGATCTTCCAAATACATAC	ENVERHIT
				CACACTCCAGTCAATGCAAAGGTTGTAAAGGACTACTACAAAATCATCACTC	LIVKNSATYNGPKHSLTQIS
				GGCCAATGGACCTACAAACACTCCGCGAAAACGTGCGTAAACGCCTCTACC	QSMLDLCDEKLKEKEDKLA
				CATCHEGGGAAGAGTTCAGAGGACCATCTGGAGCTAATTGTGAAAAAAAA	RLEKAINPLLDDDDDQVAFSF
				A A COTA CA A TEGES CON A A A CACT CATT GACT CAGA TOTO CATGO TOTO CATGO TO	LDNIVTQKMMAVPDSWPF
				CATCTCTCTCTCATGAAAAACTCCAAAGAAAAGAAAGAAA	HHPVNKKFVPDYYKVIVNP
				A A A A A A CONTACT TO THE STATE A TO A CONTACT TO THE STATE A CONTACT TO THE STATE A TO A CONTACT TO THE STATE A	MDLETIRKNISKHKYQSRES
				CATTOTO A CATTOTO A CATTOTO A CATA A A A TOTO A CATTOTO	FLDDVNLILANSVKYNGPES
				CONTROL OF THE CONTRO	OYTIKTAGEIVNVCYGTLTE
				CCATITICAL CACCOMBILITATION OF TAXABLE AND A CONTRACT AND A CONTRA	YDEHI TOLEKDICTAKEAAL
				GICAALCCAALGGAIII AAGAGAACAA AAGAAAAAAAAAAAAAAAAAAA	EEAEI ESI NPMTPGPYTPO
				ATCAGAGTCGGGGAGAGCTTTCTGGATGTTAAACCTTATTCTGGGGAGACAG	PDDI VDINITEI EMEDIAEV
				TGTTAAGTATAATGGACCTGAGAGTCAGIAIACIAAGACIGCCCAGGAGAII	PPDL1D1N1 SLSWShDASV
				GTGAACGTCTGTTACCAGACATTGACTGAGTATGATGAACATTTGACTCAACT	FODESNMSVLDIPSALPER
				TGAGAAGGATATTTGTACTGCTAAAGAAGCAGCTTTGGAGGAAGCAGAATTA	QVTQEGEDGDGDLADEEE
				GAAAGCCTGGACCCAATGACCCCAGGGCCCTACACGCCTCAGCCTCCTGAT	GTVQQPQASVLYEDLLMSE
				TTGTATAGGAAGACATCCCTCAGTATGTCTCGAGATGCCTCTGTATTTCA	GEDDEEDAGSDEEGDNPF
				A PARA GA GA A TATATATATATATATATATATATA GA GA GA GA GA GA A A A	SAIQLSESGSDSDVGSGGI
				CACCTA A CACACACACACACACACACACACACACACAC	RPKQPRMLQENTRMDMEN
				CAGGA TACACACACACACACACACACACACACACACACACACA	FESMMSYEGDGGFASHGI
				GAAGGAACI GI ACAACAACAACAA CAAGAAAAAAAAAA	EDSNISYGSYEEPDPKSNT
				TGTCTGAAGGAAGATGATGATGAAGATGCTGGGAAGTGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	OPTOFICIO CVENCEGED
				ACAATCCTTTCTCTGCTATCCAGCTGAAAGTGGAAAGTGAACTGAATGT	CDIST SSIGGILL VSELEED
				GGGATCTGGTGGAATAAGACCCCAAACAACCCCGCATGCTTCAGGAGAACAC	EEEEECHSGPSVLSQVDLS
			_	AAGGATGGACATGGAAAATGAAGAAAGCATGATGTCCTATGAGGGAGACGG	EDEEDSEDFHSIAGDSDLD
				TGGGGAGGCTTCCCATGGTTTGGAGGATAGCAACATCAGTTATGGGAGCTAT	SDE*
				GAGGAGCCTGATCCCAAGTCGAACACCCAAGACACAAGCTTCAGCAGCATC	
				GGTGGGTATGAGGTATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	
				GCGCTCTGGGCCGAGCGTACTAAGCCAGGTCCACCTGTCAGAGGACGAGG	
				AGGACAGTGAGGATTTCCACTCCATTGCTGGGGACAGTGACTTGGACTCTGA	
				TGAATGA	
æ	e	prey67316	14	CCACTCTACTCCACAAGGCTCATTCTAACTTCCCCCCTTGCTTATTIGTAACI 278	PLYS I HULL I SPLAYL-LFSL RVRPQLSLSTTYLSIYYTCS
Lodso					

HOOFERS DIFFE

			TTATTATACTIGTAGTITCAAAATTACTGAGAAAACAAATTTACTACCTAGAATA	FKITEKQIYYLEYCVNIQFSL
			CIGIGITAA ATACAATTIOLITAATTI TACAATAACAATTOOTATCAAGAGGCT TTCCAAAATTGCTTAGGTCAGCTCCTTCTCCATGCAACTGTTTCAGTGAGGCT GNATCATGGCGTTGTAATATTGTTAGAA	MOLFQ*GXIMRL*YC*
Ю	prey67318	78	CCACCGCACCTGACCTTAGITITITICTGACGTGGTCCTTCTTTTTATCTCT 279 AGACTTATGATTGCTAACACAACACACACT GGAATTGGTACTTGGGAATGCACGCTGTACTTGTAACCCAACCTT ACACATTGGTCTTGGGAATGGAGGCCTGTAGTTGTAACCCATAAGAAGA ACTGGGCCTAAGTGCAGATGAGAATCCCTGGTATAACACAACAAGA ACTGGAGATCAATGCCAATTGTTGTGATGAAACAGACAAC AACTGGAGAATCAATGCCAATGTTGTTGTGATGAACGTTTGGGGTTCCTGTGT AACTGCAAATCACAATGTTGTTTGTTATTGTAAACGTCTTGGGGTTCCTGTGT	PPHLTLVFF*RGPLLLSLRL MIAKTKDTIVTGGPWNLVL GNGGL*FVTHKRRLKGPKC R*ESLVIEGTRTGDQCG*FV MNVLGFLCDQPVGISV
<u>м</u>	prey7144	62	GGAGGCAGAAAAGCCAACCAACTCGGCTTTCAGTGGAGGCATTAAAGTAC GGAGGCCAGAAAAGCCAACTCGAGCATCATCACCGTGGGGTGGTGGCAG AGCATGAAACCCCAACACCACTACTACCCGTGGGGTGTGTGCAG TTGAGGCCATCCATCCCCAACTCTGAATCACCCAAGCTTTAACC GCAGCATCCATCCCTCCAGAGTCCTGTACAAAACTGGCCCCAAGGGTTACACC GCAGCATCCCTTCCAGCTGTTCAAAACTGGCCCCAAGGGTTGAACCG GTAGACCCCGAAACTGCTGTTCAAAACTGGCCCCAAGGGTTGAACCG GGAGAACCAAAACTGCTGTTCAAAACTGGCCCCCAAGGGTCC GTGCTCATTCCCACCTGTGTGAAACTGCTGTACACTTCCTCTTTGCACTT GGAGAATCAAACCAATAATTACTGTCAATTGGCTCTATTGCACTTTGCACT GGTGATTCGAACCACGAACTGAAGCCCCCAAGGGGGGAATC GGTGATTCGAACCACGAACTTGCAATTGACTATTGACTATTGACCATTGACACT AGCGGGGAATTGCGAACCCCAAGGGGGGAATC AGCGGGGAATTGCACCCCTCAAGGGGGGAATC AGCGGGGGAATCGCCCCAAGGGGGGAATCC AGACGAGTGGCAACTGAAGCACAATTGACCCTAAGGAACCCCCAAGGGGGGAATCC AGACGAGTGGCAACGCACCTGAAGGAAGCCCGGTAGGAAACCC AGACGAGTGGCACAGAGTTGACCCCCAAGGAATAGGAA CCACCACAGGAATAGCACATATGCCCCCAGGAATAGGAAACCCCCTAGGAAAACCG AGACGAGTGCCCCACAGAGTGA	EARKAHOLWI.SVEALKYS MATSSAEPTPIGSASAPEAI KANGSDNETOALTAAIPP ESLTRGWYSEETLRARFYA OYKLARFWAMDETRISLY OYFLSYLGSLLIPPOQUK OYFLSYLGSLLIPPOQUK GESPRAAFWOLK GESPRAAFWOLK GESPRAAFWOLK GESPRAAFWOLK GESPRAAFWOLK GESPRAAFWOLK GONG
ю	prey67328	08	ATGAAATCCCAATGGTGTAGACCAGTGGCGATGGATCTAGAGATTTACCAAC TGAGACATTTACAATTCTTTCTTGTTCTTGCTGGCGATGGATCTAGAGATTTACAATTCTTTCT	MKSOWGRPVAMDLGWQL HHFSISELSSLIGENGWB LDNSSSGASWAIDNKIEGA MDLWGSHLMYAMFEEVEVL KCOIKELIEKNSOLGCENNL LKTASPEGLAGFGANLOT GSPATTQPGGTTQPPAQ PASQGSGFTA*
<u>е</u>	prey37430	18	GTGGGAACAGGGTATACATICATICITATIAATTGCCAATGGATAGGGATATT TCATACCTTTGCGAATGAA TTCATACATTGCCAATGAA GAAGAACAAAAAATTGCAAGAGTTGCTCTTAATTTTGCCAATGAA AAGGGAATTGCAGAAAGAGAGTTACAGCCTTTTGGGCCGTCTACCAT AAGGCAATTGCAGAAAATTGCAGAATACACAGCAATAGATTACCAGTTACATA GCCTACAGTTGAAAAATTGCAGAAATACAACAACAAATAGATTTTATGGTC CACAAGTCAATTAACCAAGGAAATTAGCAAGAAAAATAGAACAACAAATAGAATTTGCAGCAA ATTGCACATTTACCAGGGAAATATAGGAACACAAATACAACAGGAAATTGCAAGCAA	WECELYNHYWSPRSPGYF HTFADDTCOVALNEANEE AKKFRKAYTDLIGHRORKS EKRADPORGNILWATVOI KNPETTNHFVGPOVNNISH GTPSNFCHIGHVGWDPNT GSDLNNLDPELKNLFDMCG

-			ľ	TCCASAATTGAAGAATCTTTTTGATATGTGGAATCTTAGAGGCACAACTTA	ILEAQLKERETLKVIYDFIEK
				AAGAAAGAAACATTAAAAGTTATATATGACTTTATTGAAAAAACAGGAGGT	TGGVEAVKNELRRQAPPP
				GTTGAAGCTGTTAAAAATGAACTGCGGAGGCAAGCACCACCACCACCACCAC	PPPSRGGPPPPPPHSS
				CATCAAGGGGAGGGCCACCTCCTCCTCCCCCCTCCACATAGCTCGGGTC	GPPPPARGRGAPPPPS
				CTCCTCCTCCTCCTCCTGCTAGGGGAAGAGGCGCTCCTCCCCCCACCACCTTCAA	RAPTAAPPPPPSRPSVEV
				GAGCTCCCACAGCTGCACCTCCACCACCCTCCTTCCAGGCCAAGTGTAG	PPPPPNRMYPPPPALPSS
				AAGTOCOTOCACCACCAAATAGGATGTACCCTCCTCCACCTCCAGCCCT	APSGPPPPPSVLGVGPVA
				TOCCTCCACCATCAGGGCCTCCACCACCACCACCACCACCACCACCACCACCACCAC	PPPPPPPPPGPPPPGL
				GGTAGGGCCAGGGCACCACCCCACCGCCTCCACCTCCACCTCCTGG	PSDGDHQVPTTAGNKAALL
				GCCACCACCACCACCACCACCATCACATGGGGACCATCAGGTTCCAAC	DQIREGAQLKKVEQNSRPV
				TACTGCAGGAAACAAAGCAGCTCTTTTAGATCAAATTAGAGAGGGTGCTCAG	SCSGRDALLDQIRQGIQLK
				CTAAAAAAAGTGGAGCAGAACAGTCGGCCAGTGTCCTGCTCTGGACGAGAT	SVADGQESTPPTPAPTSGI
				GCACTGTTAGACCAGATACGACAGGGTATCCAACTAAAATCTGTGGCTGATG	VGALMEVMQKRSKAIHSSD
				GCCAAGAGTCTACACCACCAACACCTGCACCCACTTCAGGAATTGTGGGTG	EDEDEDDEEDFEDDDEWE
				CATTAATGGAAGTGATGCAGAAAAGGAGCAAAGCCATTCATT	, 0
				AGATGAAGATGAAGATGAAGAAGATTTTGAGGATGATGAT	
				GAUIGA	IAEUVVCDGAI GBVEI EI I I
Shigella 3	_	prey67351	82		A DAVODI TI OCIDE
ospC1				TTGCTGCTTTGACTCCCTGCCGCGCCCCCTTACTTACTCTGC	
				CTACCAGGTTTTCCATTTCCAGGCAGTCTTTCTAATTTTCCACCTGGAAG	VEST TITE TITE TO THE TITE TO
				AAACTTTCTTTTCTCTGAGTTCGTAATCTTATAATAAGTACCTATTTTTCTCTTC	IL**VPIFLFF*HI*NVLSDVSS
				TTCTAGCGTATATAAAATGTATTATCTGACGTGTCAAGTGAGTTAATGCATTTA	ELMHLKSLGMVP
				AAGAGCCTAGGAATGGTACCTAC	
Shigella 3		prev67353	83	GGAGAAGAGAGGGAGCAACTCGGTATTTGTCCACAAAAAGAGTATTATTCCA 284	EKRGSNSVFVHKKSIIPEEE
				GAGGAAGAGTGTTATATAAATTGTGTTTTCCAATAAAAATAGTGATGTCTATC	CYINCVFQ*K***CLSVQC1W
				AGTTCAGTGTACATGGACCTTTGCAGTGAGTCAGAGATTTGGCCTAGGCCTG	TFAVSQRFGLGLWGISLGE
				TGGGGGATATCCCTGGGAGAAACTGTCTTGTCAAAGGAAGTTAGCATTTGAG	TVLSKEVSI*DDGMIFAHLS
				ACGATGGCATGATCTTTGCCCACTTATCCCATCAAAAAGAGTTTTGAAAGGAT	HQKEF*KDSXEALI*XATL
Shinella 3	3	prev25185	84	GGCTGCCCTGCCTGATGACATCCGTCGGGAAGTTCTACAGAACCAGCTAGG 285	AALPDDIRREVLONOLGIRP
			_	CATTCGTCCACCAACCCGGACTGCCCCCTCCACAAATAGCTCAGCGCCTGC	PTRTAPSTNSSAPAVVGNP
0				AGTGGTGGGGAATCCTGGTGTGACTGAAGTGAGCCCTGAGTTTCTGGCTGC	GVTEVSPEFLAALPPAIQEE
				CCTGCCTCCAGCCATTCAGGAGGAAGTACTGGCACAGCAGAGAGCTGAGCA	VLAQQRAEQQRRELAQNA
				GCAGCGACGAGAACTAGCACAGAATGCCAGCTCAGACACCCCTATGGACCC	SSDTPMDPVTFIQTLPSDL
				TETGACCTTCATCCAGACTCTGCCCTCAGACCTGCGCCGTAGTGTCCTAGAG	RRSVLEDMEDSVLAVMPP
				GATATGGAGGACAGTGTGTTAGCTGTGATGCCACCTGACATTGCAGCTGAG	DIAAEAQALRREQEARQRQ
				GCTCAAGCCCTGAGACGAGAGCAAGAAGCCCGGCAGCGACAGCTCATGCAT	LMHERLFGHSSTSALSAILR
				GAGCGTCTGTTTGGGCACAGTAGCACCTCCGCACTCTCTGCTATTCTCCGAA	SPAFTSRLSGNRGVQYTRL
				GCCCGGCTTTCACCAGTCGCTTAAGTGGCAACCGTGGGGTCCAGTATACTC	AVQRGGTFQMGGSSSHNH

OLSLDELWDMLGECLKELE WVIRSLLSILORSSESELCIE VLDTLIQLAKVFPSHFTQQR **VPVSAGGEGETSPYSLEAS** SEACANSGSGASSTTTATS TTSTTTTAASTTPTPPTAP **TPVTSAPALVAATAISTIVVA** DFKMVSSGLTENQLQLSVE **ELREYNLEQORRAQCETLS** OSBFDMAENVVIVASOKRP GGRELOLPSMSMLTSKTS VDQPSPSAQDTQSIASDGT ESHDQHAVLVLQPAVEAFF LVHATERESKPPVRDTRES SGGSTVHIHPQAAPVVCRH **FOKFFLRVLQVIIQLRDDTR** POGEKEKEERPPELPLLSE HEALSCLLVLLFVDEPKLNT TPKLTTSEEKGKKSSKSCG SSSHENBPLDLLHKMESKS SNOLSWLSVSMDAALGCR PLGQLMNMLSHPVIRRSSL VLTSHSCSEEGLEDAANVL PDGLPEEOPOTTKLKGKM RANKKAKQTGRLGSSGLG **PSGSNVDTLLRLRGRLLLD INIFQIQRSGGRKHTEKHA** PCSSOSSSSGICTDFWDLL VKI DNMNVSBKGKNSVKS TEKLLRLSLISIALPENKV ASTTVTTPTTATTVSISPT LOLSRGDSGTRDTVLKLLL NGARHLGYTLCKQIGTLLA SASSIQAAVRQLEAEADAII QMVREGQRARRQQQAAT SESSOSEASVRREESPMD SRLHRVLRNLCYHAGTRH TKETNCESDRERGNKACS TKGSKSPAKVSDGGSSST GGCAAAATGCAGAGCAGGTTTGACATGGCTGAGAATGTGGTAATTGTGGCAT GGCTCCTTCTGGACCACGAAGCCCTTTCTTGTCTTGGTCCTACTTTTTGTG CAGCTTTCCTGGCTCTCAGTATCCATGGATGCAGCCCTAGGCTGCAGGACTA GCAATAAGGCCTGTAGCCCATGCTCCTCACAGTCCTCCAGGGCAGTTTG CTCAGACTCCTTTCTCTCATCTCAATTGCTCTCCCAGAAAACAAGGTGTCAGA TACTGCACCCACCCCTGTCACTTCTGCTCCAGCCCTGGTTGCTGCCACGGCT CTACCACTACTGTTTCAATTTCTCCCACTACTAAGGGCAGCAAATCTCCAGCG CTTGTTCTGAGGAAGGCTTAGAGGATGCAGCCAACGTACTACTGCAGCTCTC CCGGGGGGGACTCTGGGACCCGGGACACTGTTCTCAAGCTGCTACTGAATGG GAGCTGCGGGAATACAACCTCGAGCAGCAGCGGCGAGCCCAATGTGAAACC CATCATCCAGCTCCGGGACGACACGCGCCGGGCTAACAAGAAAGCCAAGCA CATAACAGGCCTTCTGGCAGTAATGTAGATACTCTCCTCCGCCTCCGAGGAC GCAGCGCAGCAGTGAGATGAGCTATGCATTGAAACACCCAAACTCACTACA ATATATTCAGATCCAGCGTTCAGGGGGGGCGTAAACATACCGAGAAGCATGC CAGACACGTTTTGGATACACTCATTCAATTGGCCAAGGTATTTCCCAGCCACT AGCCCGCCATCTGGGTTATACCCTTTGTAAACAAATAGGTACCCTGCTGGCC CTCAGAAGCGACCTTTGGGTGGCCGGGAGCTCCAGCTGCCTTCTATGTCCA GACAGGCAGGCTAGGTTCCTCCGGTTTAGGCTCAGCTAGCAGCATCCAGGC TCACACAGCAGCGGACCAAAGAAACAAACTGTGAGAGTGATCGGGAAAGGG CACAGACTTCTGGGACTTATTGGTAAAACTGGACAACATGAATGTCAGCCGG GGAAACCTCTCCATACAGCCTCGAGGCCTCTCCACTGGGGCAGCTCATGAA CATGITGICACACCCAGICATCCGCCGGAGCICTCTCTTAACTGAGAAACTC ATTTCCACCATTGTCGTAGCTGCTTCGACCACAGTGACTACCCCCACGACTG GGCCTCACTGAAAACCAGCTACAGCTCTCTGTAGAGGTGTTGACATCCCACT CTCTCTCCTGATGGCCTGCCTGAGGAGCAGCCACAGACCACCAAGCTGAAG IGTTGACATCCAAGACATCTACCCAGAAGTTCTTCTTGAGGGTACTACAGGT AGCTGTTCGGCAGCTGGGGCTGAGGCTGATGCCATTATACAAATGGTACG GATGAGCCAAAGCTCAATACTAGCCGTCTACACCGAGTACTGAGAAATCTCT GCTACCATGCCCAGACCCGCCACTGGGTCATCCGCAGTCTGCTCTCCATCT AGTGAGGAAAAGGGCAAAAAGTCGAGCAAGAGCTGTGGGTCAAGTAGCCAT GAGAACCGTCCCCTGGACCTGCTACACAAGATGGAGTCAAAGAGCTCCAAC AAGCGGTGGCTCCACCGTCCATCCATCCCAAGCTGCTCCTGTTGTCTG AAAGGCAAGAACTCCGTGAAGTCAGTGCCAGTGAGCGCTGGCGGTGAGGG AGCACAGGCTAATTCTGGCAGCGGTGCTTCCTCCACCACCACTGCCACCTC AACCACATCTACCACCACCACCACTGCGGCCTCCACCACGCCCACACCCCC AAGGTGAGTGATGGGGGCAGCAGTACAGACTTTAAGATGGTGTCCTCT TGAGGGTCAAAGGGCGCGGAGACAGCAACAAGCAGCACGTCGGAGTCTA **3CCAGTCAGAGGCGTCTGTCCGGAGGGAGGAATCACCCATGGATGTGGAC** GCCTTGCTGTGCAGAGAGGTGGCACCTTCCAGATGGGGGGGTAGCAGCAGC

RKCSQHNRLREFFCPEHS	CCGCAAATGTTCCCAGCACAATCGGCTGCGGGAATTTTTCTGCCCCGAGCA 286	82	prey4411	8	Shigella
	CGCGCCTGTTTCTCACCTTCTCCCCTTTCCATGCCGTCCATGATCCCC ACCCCATGTGTTTTAAAAAGGCAGTAG				
	AAGAAATTGTCAAAAACCAATAAATGAAATCCACCACCACTGACCGTGTGTGT				
	TTTTTTACCATTGTTGGACCTGGGGAGGGGGGGGTTAAAAAAAA				
	TATGAGAGCTTTGAGAAGTCCGCCACATGCTACTGTTGGCTATCCAGGGT CTCTGAAGGCTTTGGGCTGGCCTAATAAGGCCCTGCCCAACTCCGTGGGGT				
	AGATCGCCTGCCTTCAGCTCACACATGTTTTAATCAGCTGGATCTGCCTGC		_		
	AAGGCATGAATGGCATTCAGAAGTTTCAGATCCATCGAGATGACAGGTCCAC				
PLSMPSMIPTPCVLKRQ*	CAGTITIGICACGGGTACTICCAAGGTACCCCTGCAAGGCTTTGCTGCCCTCG	_			
AHTCSSSHSLPAACFLTFS	AATCCAACACTGAATACCACAAGTTCTTTCGATCAAGCTGACGTGTGCCAAGTTCCTC				
PLLDLGHGELKKEPERNCQ	GAGTTAGAGCTGCTTATATCAGGACTGCCCACCATTGACATCGATGATCIGA	_			
LKALGWPNKALPNSVGFFL	AAGGCTTCTATGAGATCATTCCAAAGCGCCTCATTTCCATCTTCACTGAGCAG				
AYESFEKSATCYCWLSRSA	GCCAACATGAGAATGACAGGAGCCATCCGCAAGCAGTTGGCGGCTTTCTTAG			_	
PAALEGMINGIQKFQIHHDD	TGAGGTCCAAGAGTTTGGAGTTTGTGAAGTTCGTGACCTCAAACCCAATGGG			_	
DRAKFLOFVTGTSKVPLQG	ATCTGCTGGAAAATGATGTCTCCACACTAGGCTATGACCTCACCTTCAGCAC				
SNSIQIQWFWRALRSFDQA	CAGATATACAGATATGGAGAGTGAAGATTACCACTTCTACCAAGGTCTGGTTT				
SEIPKRLISIFI EGELELLIS	CTTCAAGTTTGTCGGACGCATTGTGGCCAAAGCTGTATGTGGCAACCGTC11				
QMRIMTGAIRKQLAAFLEGF	TCACCTACACCATCAATCCATCTTCCCACTGCAACCCCAACCACCTCAGCTA				
GANILVTEENKKEYVHLVC	GAGATGTTTAACCCTATGTATGCCTTGTTCCGTACCTCACCTGGTGATCGAG				
FSTEVQEFGVCEVRDLKPN	AATICOCCGGAAGAAATGAAGAAATTGAATTGATTATTTATTGATGAT				
OGLVVI ENDVSTI GVDI T	CATGTCCGTCGTGACCATGTGTGTGTGTGTTTTTTTTGTATTTCAAGAAGAA				
AVYDNRLLECYFTRSFYKH	CAAGAGCTGGAGCGTTTAGATGAGGGGCTCCGGAAAGAAGAAGAGGTGTG				
HCNPNHLSYFKFVGRIVAK	GGTAGACTACATTCGTGTCCTCGACTTTGATGTCAAGCGCAAATATTTCCGC	_			
YALFRTSPGDRVTYTINPSS	AGATCCTACGGCAGTCCACGACCCACCTTGCTGATGGGCCTTTTGCTGTCCT				
GGLLREWYMIISREMFNPM	ATTOLIC COUGGGGAGCCC CATOCACACA CATOCACACACACACACACACACACACACACACACACACA				
VERDINATEDSYNELHINGSP FEMKNRI VIVERGEFEGODA	CTCCACTCTCCCCTGCCCCCTTAACCCCAGCCACGCCTTCCTCCCTTGACCCCTT				
QELERLDEGLRKEDMAVH	CTGTCCGAGACACCCGTGAGAGCCAGCTGGCACACATCAAGGACGAGCCTC	_			
VLVDYIRVLDFDVKRKYFR	CTGTCGAGGCTTCTTCTGGTCCATGCCACAGAGCGGGAGAGCAAGCCTC				
VLNQILRQSTTHLADGPFA	AGGAACTAGAGGAATCCCATGACCAGCATGCGGTGCTAGTGCTACAGCCTG				
SSLPPDTQKFLRFAETHRT	CACAGGGGGAGAAGGAAAAGGAAAAGAAAAAAAACAACTTGGGGAGTGGTAAA				
TPSSLDPFFSBEPSSMHIS	CAGCCATCTCCCAG GC CAAGA ACI CAA CCA I GCC CCGA I GGAACCC				

KODESHOY DIZION

			CARCOLARTOTACCACATCTGCCTGGTGGAGCATAAGACCTGCTCTCC	ECICHICLVEHKTCSPASLS
osbo			CACCATCCTTGAGCCAGGCCAGCGACCTGGAGGCCACCTGAGGCACA	QASADLEATLRHKLTVMYS
			AACTAACTGTCATGTACAGTCAACGGGGGGGCGTCGAGAGCACTGGATG	QINGASRALDDVRNRQQD
			ATGTGAGAAACAGGCAGCAGGATGTGCGGATGACTGCAAACAGAAAGGTGG	VRMTANRKVEQLQQEYTE
			AGGAGGTACAACAAGAATACACGGAAATGAAGGCTCTCTTGGACGCCTCAGA	MKALLDASETTSTRKIKEEE
			GACCACCTCGACAAGGAAGATAAAGGAAGAGGAGAGAGAG	KRVNSKFDTIYQILLKKKSEI
			GTTTGACACCATTTATCAGATTCTCCTCAAGAAGAAGAGTGAGATCCAGACCT	QTLKEEIEQSLTKRDEFEFL
	-		TGAAGGAGGAGATTGAACAGAGCCTGACCAAGAGGGATGAGTTCGAGTTTC	EKASKLRGISTKPVYIPEVE
			TGGAGAAAGCATCAAAACTGCGAGGAATCTCAACAAAGCCAGTCTACATCCC	LNHKLIKGIHOSTIDLKNELK
			CGAGGTGGAACTGAACCACAAGCTGATAAAAGGCATCCACCAGAGCACCAT	QCIGRLQELTPSSGDPGEH
_	-		AGACCTCAAAAACGAGCTGAAGCAGTGCATCGGGCGGCTCCAGGAGCTCAC	DPASTHKSTRPVKKVSKEE
-			CCCCAGTTCAGGTGACCCTGGAGAGCATGACCCAGCGTCCACACACA	KKSKKPPPVPALPSKLPTF
			CACACGCCCTGTGAAGAAGGTCTCCAAAGAGGAAAAGAAATCCAAGAAACCT	GAPEQLVDLKQAGLEAAAK
			CCCCCTGTCCCTGCCTTACCCAGCAAGCTTCCCACGTTTGGAGCCCCGGAA	ATSSHPNSTSLKAKVLETFL
			CAGTTAGTGGATTTAAAACAAGCTGGCTTGGAGGCTGCAGCCAAAGCCACCA	AKSRPELLEYYIKVILDYNT
			GCTCACATCCGAACTCAACATCTCTCAAGGCCAAGGTGCTGGAGACCTTCCT	AHNKVALSECYTVASVAEM
			GGCCAAGTCCAGACCTGAGCTCCTGGAGTATTACATTAAAGTCATCCTGGAC	PONYRPHPORFTYCSOVL
			TACAACACCGCCCACAACAAAGTGGCTCTGTCAGAGTGCTATACAGTAGCTT	GLHCYKKGIHYWEVELQKN
			CTGTGGCTGAGATGCCTCAGAACTACCGGCCGCATCCCCAGAGGTTCACAT	NFCGVGICYGSMNRQGPE
			ACTECTCTCAGGTGCTGGGCCTGCACTGCTACAAGAAGGGGATCCACTACT	SRLGRNSASWCVEWFNTK
			GGGAGGTGGAGCTGCAGAAGAACAACTTCTGTGGGGTAGGCATCTGCTACG	ISAWHNNVEKTLPSTKATR
			GAAGCATGAACCGGCAGGGCCCAGAAAGCAGGCTCGGCCGCAACAGCGCC	VGVLLNCDHGFVIFFAVAD
			TCCTGGTGCGTGGAGTGGTTCAACACCAAGATCTCTGCCTGGCACAATAACG	KVHLMYKFRVDFTEALYPA
		_	TGGAGAAAACCCTGCCCTCCACCAAGGCCACGCGGGTGGGCGTGCTTCTCA	FWVFSAGATLSICSPK*
		_	ACTGTGACCACGGCTTTGTCATCTTCGCTGTTGCCGACAAGGTCCACCT	
			GATGTATAAGTTCAGGGTGGACTTTACTGAGGCTTTGTACCCGGCTTTCTGG	
			GTATTTCTGCTGGTGCCACACTCTCCATCTGCTCCCCCAAGTAG	
Shigella 3	prey2686	98	ATGGAGCAGCTGGCCGACGTGACGCTGCGAAGGCTGCTGGATAATGAGGTC 287	MEQLADVI LARLLUNEVFU
ospC1			TTTGACCTCGACCCCGATCTGCAGGAGCCGAGCCAGATCACCAAGAGGAC	ACNIECEBACEDI DEVEKI IL
			CTGGAAGCCAGAGCACAGAATGAGIICIICCGGGGCIIICIICAGGIIGCCGA	ACIDED IN THE PROPERTY OF THE
			GGAAGGAGAAGCTGCACGCGGTTGTGGACTGTTCGCTCTGGACGCCGTTCA	AVVDCSEWIFFSHORING
		_	GTCGCTGTCACACCGCGGGGGGGGATGTTCGCCTCTGACAGCTACATCIGCT	HMFASUS YICFASHEDGCC
			TTGCCAGCAGAGAGATGGCTGCTGTAAGATCATCCTGCCAC1CAGAGAGG	KIILPLAEVSIENMEDISLI PHDIIVSIDSKVAEOFIEI BD
			TGGTGAGCATCGAGAAGATGGAGGACACGAGCCIGCIGCCGCAICA	DOC! VEA! ABI KOVHANH
		_	TTGTCAGTATCAGAAGCAAGGIGGCCIICCAGIICAIIGAGCICCAGGAACCG	DVHYDTSADDDMASI VEHS
			AGACAGCC GG GGAGGCGC GC I GC I GC I GAAGCAGG CAACACAG CAACACACAG CAACACAG CAACACACAG CAACACAG CAACACACACAG CAACACACACACAG CAACACACACACACACACACACACACACACACACACA	TSWCSDHBEGDI EMMSSO
			ACCACCCGTGCACI ACGACACCICI GCGGAIGAI GACAI GGCI I CACI CGI	NSEESEKEKSPI MHPDAI V
_			GTTTCATTCAACAAGCATGTGCAGTGACCACAGAGATTTGGGGGATCTTGAAAAAAAA	TAFOOSGSOSPOSBMSBE
			A GIOI CI CARAA I AGCGAGGAGAGI GAGAAAAGAAAAAAAAAAAAAA	555555555555555555555555555555555555555

SAPSPEDSVFADTGKTPQD WELT FLISHMPLESAVNVVD PNGDAVDYQKQLKQMIKDL AKEKDKTEKELPKMSQREF GBI WILFSDAVTDLASHPG ERDLHRSLPEHPAFONETG COSMNILTSVLLLYTKEEEA RDSYEKFGDQSVEQIEHLR YKHRIRVLOGHEDTTKQNV LRVVIPEVSILPEDLEELYDL ASBHDPSRPYAFOYBIDAR EILAERTFRLLDDNMDQLIE FKAFVSCLDIMYNGEMNEK SQALPEAAERDWTVSLEHI MFRTEKIRKLVAMGIPESLR AYGNL VEESL GKCCL VTEEL **PELAEHMNDLSALASVSLS** NAEDLCSSKDDGQALMILS RFLDHIKNEDSPGPPVGSH HAFFSDDQEPYPVTDISDLI FKREHMMSCYWEQPRPM **QSPLRNPLLSTSRPLVFGK** IGFCKTLYSMFHEDPEEND LYGAIATVTTLLLQIGEVGQ RGSSSGSCSQECGEELRA GIKISLWNDHFVEYGRTVC AALRRVLTAYAHRNPKIGY **FWLLVAVCERMLPDYFNH** RVIGAQVDQSVFEELIKGHI CFFYDGIKAIFQLGLAVLEA **QFAHLFQLVSPWTCGAHT IKLLYRLHIPPALTENDRDS** ASLLTEQSLVNFFEKPLD MKSKLENAKINQYNLKTFE MSHQSQSELKLSNL* GGGCTTCAGCTCCTTCTCCTGAGGACTCGGTTTTTGCAGACACTGGGAAGAC TCTCCCTTGAACATATTTAGCTTCACTTCTGACTGAACAGTCATTAGTCAACT TCCTCAGCAGGTTTCTAGATCACATTAAGAATGAGGACAGCCCAGGGCCCCC GTTCCTCAGCATCATGCCTCTAGAGAGAGTGCGGTGAATGTGGTAGACTGCTTC TCTATGATGGCATCAAAGCCATCTTCCAGCTGGGACTGGCTGTGCTTGAGG GAGAAATGAATGAGAAGATTAAACTATTATACAGGCTTCATATCCCTCCAGCA CTCACTGAAAATGACCGAGACAGCCAGTCGCCGTTGAGGAATCCTCTGTTGT CAACATCGAGACCCCTGGTTTTCGGGAAACCCAATGGTGATGCAGTTGATTA GCGAGGCAGCTCTGGAAGCTGCTCCCAGGAGTGTGGGGGAGGAGCTGC TTTTGAAAAGCCACTGGACATGAAATCCAAACTTGAAAATGCCAAGATCAAT TTGTGGAATACGGCAGAACCGTGTGTATGTTTCGCACAGAGAAGATTCGGAA CTTCTCAGATGCGGTGACGGATCTTGCCTCACACCCTGGTTACTACGGGAAT CTGGTGGAGGAGTCCCTGGGGAAATGCTGCCTGGTAACCGAGGAGATAGAA CGAGACCTGCACCGCTCCCTGCCAGAGCACCCCGCCTTCCAGAACGAAACG AAGATTGGATACTGCCAGTCCATGAACATCCTGACCTCCGTGCTGCTGCTGT TGAACGACCTCTCAGCCCTGGCGTCTGTCTCTCTCGTGGTTCCTGACCCT CCAATGCTGAGGACCTGTGCAGCAGGATGATGGTGGCCAGGCCTTGATGA GACTGATATTCGGACCTGATCCGGGATTCCTATGAGAAATTTGGAGACCAG GAGAACATATGATGAGCTGTTACTGGGAGCAGCCCAGGCCCATGGCCTCAC CAGTTTGCACACCTGTTTCAGCTAGTCTCGCCCTGGACCTGCGGGGCCCAC ACGGAGATCCTCGCCGAAAGGACGTTCAGGCTCTTGGATGACAACATGGAC AAACTCTGTACAGTATGTTCCATGAAGATCCAGAAGAAAATGATTTGTATCAA GCCCCAGGACTCCCAGGCACTTCCAGAGGCGGCAGAAAGGGACTGGACTG CACCCGATGCCCTGGTCACCGCCTTCCAGCAGTCAGGCAGCCAGAGCCCT GGAATTGCTGCTTTGAGGAGAGTCTTGACGGCCTATGCCCACCGGAACCCC CTGTCTTCGAGGAGCTCATCAAGGGTCATCTCCCAGAGCTGGCAGAGCACA AGTTGGCAGCCACCATGCCTTTTTCTCCGACGACCAGGAGCCCTACCCTGT TCTGTGGAGCAGATCGAGCACCTACGTTACAAGCACAGGATCAGGGTCCTC CAAGGCCACGAGGACACCACAAAGCAGAACGTGCTTCGAGTCGTTATCCCG GAAGTCTCAATTCTTCCTGAAGACCTAGAGGAGCTCTACGACTTATTCAAGA GCCACGACCCCAGCCGGCCCTATGCTGAGCAGTACCGCATAGACGCCCGG CAGCTCATCGAGTTCAAAGCGTTTGTGAGCTGCCTCGATATTATGTATAATG TCAGAAACAGCTGAAGCAGATGATTAAGGATTTAGCCAAAGAAAAAGATAAA ACTGAGAAAGAATTGCCCAAAATGAGCCAGAGAGAATTTATCCAGTTCTGTA GCCATCGCCACAGTCACCACACTGCTGCTGCAGATCGGGGGAGGTGGGGCA GACTCCCGAATGTCCAGAGAACAGATAAAAATAAGCCTGTGGAATGACCACT FIGCTGCCCGATTACTTCAACCACCGAGTGATCGGGGCCACAAGTTGACCAGT GCTCGTAGCCATGGGCATCCCTGAATCTTTGCGAGGGAGACTCTGGCTTCT

IDDIBLEY DATION

				CAGTACAATCTCAAAACTTTTGAAATGAGCCACCAATCACAATCTGAACTTAA	
Shigella ospC1	e e	prey67368	87	AGGANCCOTACTACCAGCCACCTACACCACTGGT TCCTTTGCATCTACCAGCAGCCACCTACACCACTGGC CANCTITACGTACAGAGATGGCTTGATCAGGCAGTGGC CANCTITACGTAGAGAGATGGCATAGTTGGGTTTCC CANCTITACGTTAGAGATGGGCATAGATGGGTTTCC CANCTITACGTTAGAGATGGACTAGTAGTGGTTTCC AGGCCCATGGTTTCCTAACGATTTCATTCTGATTCC AGTAGTAGTTGTTGCATTCTAACGATTTCATTCTGA CANCTITCTACTCTCAACAGACATGCAACTGA CAGAGCTGCAGCACTGGGACCGGCAACTGAA AAAAACGCGCGCTGGAGCATTAGCCTTGAA AAAAACGCGCGCTGGAGCAATTGCCTTGAA AAAAACGCGCGCTGAACATGCCTTGAA AAAAACGCGCGCTGAACAACCTTCTCAACAGCAGGAGGACC AAAAACCCGCGCTGAACAACCTGAACCTTCTCATGA CAGTTCTCAAGTCCAACAACCAGCACATTCCTTCATGAACTCTCTCT	I IPDPLOERVOPPYTINE ITGN.LHPEWSLATGWRFK RRPGIETLEOQLAPIYEWIF RSTEMATA-PELISVOPHG RSYRLENDATRYMDGHW ROJSGLWIPDRATRYWDCK KAFILOPYNGWALIPWU GNSDDRAULDISAFLKTIAL ROYEDVATVLEHPALEDP LAAFKGROSRIEDGEGOA LAAFKGROSRIEGEEGOA ABELSKSWKONLFLGSITS ARIUPRISKONLFLGSITS ARIUPRISKON
Shigella sport	ю 	prey67371	88	588	WGYGMGH-VXXXX-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Shigela	м	prey4005	68	TIGGATOTGAGACOCTOTTGAGAGG 280 STOCKAGATGG 280 STOCKAGATGG 280 STOCKAGATGGAGG 280 STOCKAGATGGAGG 280 STOCKAGATGGAGG 280 STOCKAGATGGAGG 280 STOCKAGATGGAGGAGG 280 STOCKAGATGGAGAGGAGGAGGAGGAGAGGAGAGGAGAGGAGA	SINISTINGENT OF SERVINGENT OF

HODESENT OFFICE

			GCAGAAGTGGGCATCTCGGAGCCAGCCTGGAAGCTTCAGCAGGGCTATC CCCACACOCCTACCOACTGGAAAGGAGTGTTGTAAGACTAGGTTTTGGCTA A	FG*
Shigella 3 ospC1	prey67380	06	NININININININININININININININININININI	XXXXXXXXXXXXXXXXSLCIF F-WYLCFIIHTY*IKSEQ*LC AK*!LLSILAKKS*WSRMISP GHLYCSQVSNSFLGAKTSG FTLXLVNILKXYX
Shigela spC1	prey/2996	6	GGAGCOTRICTORAGIGGACACGGCCGAACAMCOTCOTTTGACTTORAGICTORAGICTORAGICAGGCCGGACAAT TGCCCAACAGGCCGAACAMGCTGGAACGGCGCGGACAAT TGCCCAACTGCTGCACCTCTTAACAGGCGCATCAACTTGACTTGACT AACACTGCCACCTGTGCATTGACGGCACACATCAACTTGACGACAT TTGCTGTCTACCACAGATTGACGGCACTGACTTGACT	PONSOTRIENIE ESRAK ENLPSKAGEGRATMITVI DPKRITAMINGLITIEPAVIM CAALLIN DEFANSKOGIEKU LIMMATEEEROKIGEGAOLA NEDPLEAGEREN LAMILASIG GLARHCAUN AFKLODISA ERIAREL FOLKOMEOLU SOSOSGEELSYLEKOSOW ERIAREL FOLKOMEOLU SOSOSGEELSYLEKOSOW DYRROGALHHICSVLVO PRESSOLY SEIPALT ROAW DFCOLTEN GOLERSRAA ERSEN SOSOSGEELSYLEKOSOW OFFICIAL TROAM DEFOLTEN GOLERSRAA ERSEN SANGERAL ARAR ITH-LOOGARIVAMILRIVH ENTORHEN LEEVES OVGERANDEN PROVANSE SOSIWET DITHEFER OFFICIAL BEFU EYRT CREPAU COCONOCAT YRENNYTR GRANTETEKF SONGERANDEN SOSOW SOSIWET ON SOSOW TRESS PRALAR FREKRSON NIKSS PRALAR FREKRSON NIKSS PRALAR FREKRSON NIKSS RAHLANGEGODLVO ALGISK GPGLEV
1		-		

TOOKSHEY COLITOR

Shidella	60	prev2108	92	GCAGGAAGCTCAGAGTATCGATGAAATCTACAAATACGACAAGAAACAGCAG 293	QEAQSIDEIYKYDKKQQQEI
	_			CAAGAAATCCTGGCGGCGAAGCCCTGGACTAAGGATCACCAIIACIIIAAGI	ALANT WINDHILL INTO THE
				ACTGCAAAATCTCAGCATTGGCTCTGCTGAAGATGGTGATGCATGGTGATGGTGATGGTGATGGTGA	MGLMLGKVDGETMIIMDSF
				GGGAGGCAACTTATGGACAGTTTTGCTTTGCCTGTGGAGGGCACTGAAACC	ALPVEGTETRVNAQAAAYE
				CGAGTAAATGCTCAGGCTGCTGCATATGAATACATGGCTGCATACATA	YMAAYIENAKQVGRLENAI
				AT A TACA A A CA A GA GA GA GA GA GA A TACA A TACA A A TA	GWYHSHPGYGCWLSGIDV
				CCTGGCTATGGCTGCTTTCTGGGATTGATGTTAGTACTCAGATGCTC	STOMLNOGFOEPFVAVVID
				AATCAGCAGTTCCAGGAACCATTTGTAGCAGTGGTGATTGAT	PTRTISAGKVNLGAFRTYP
				CAATATCCGCAGGGAAAGTGAATCTTGGCGCCTTTAGGACATACCCAAAGGG	KGYKPPDEGPSEYQIIPLN
				CTACAAACCTCCTGATGAAGGACCTTCTGAGTACCAGACTATTCCACTTAATA	KIEDFGVHCKQYYALEVSY
				AAATAGAAGATTTTGGTGTACACTGCAAACAATATTATGCCTTAGAAGTCTCA	FKSSLDHKLLELLWNKYWV
				TATTTCAAATCCTCTTTGGATCGCAAATTGCTTGAGCTGTTGTGGAATAAATA	NILSSSSLLINADY I GQV
				CTGGGTGAATACGTTGAGTTCTTCTAGCTTGCTTACIAATGCAGACIAIACCA	FULSERLEGSEAGLGHGSF
				CTGGTCAGGTCTTTGATTTGTCTGAAAAGTTAGAGCAGTCAGAAGCCCAGCI	MLGLE I HURKSEUNLANA!
				GGGACGAGGAGTTTCATGTTGGGTTTAGAAACGCATGACCGAAAATCAGAA	RUSCAL LIEAINGLAIN
				GACAAACTTGCCAAAGCTACAAGAGACAGCTGTAAAACTACCATAGAAGCTA	DKLFNQINIS"
				TCCATGGATTGATGTCTCAGGTTATTAAGGATAAACTGTTTAATCAAATTAACA	
					MONONO* IDOLOGIO II TO I
Shinella	m	prev67403	93	TTGGGGCATCTTGGCAGGAGCTTTGGATTTCTTTAGGGAAATGGCAATCAGA 294	CONCRETE GIVENORIA
n Conso	_			TGGGGCAGAGTGTTTTTTGCTGAGGGAATCAGAATGATCCCTCAAACAGCAC	GOSVFC GNONDESNS IF
2				CTTTGATCTCTATTCTCTGCTAAAGATGGTGCTTCCTCTACTTCCCCAGACCC	DLYSLLKMVLPLLPQ1Pvsv
			_	CCGTGTCTGTTCCATTCCATGAATTTTTCATCAGGGTCACAGGACAAAGGTT	PFP*IFHQGHRTKVLVFGSN
				TTAGTCTTTGGTTCTAATGAGACCTCTGACTTGGCTCTGGATGACTATGAAAC	ETSDLALDDYETSECICLF
				TAGESATECATTTGTCTTTTCTGGAATCCN	WNP
1		27405	2	ACTAVATATEGTAGGTATTGATAGCTTACTATGTATCAGATCCNNNNNNNNNN	ANMVAIDSLLCIRSXXXXXX
Suigella	0	preyor too	5	NUNNUNNUNNUNNUNNUNNUNNUNNUNNUNNUNNUNNUN	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
osbo				MANNANNANNANNANNANNANNANNANNANNANNANNANN	XXXXXXXXXE*LGLQW*A
				GCTAGGACTACAGTGGTGAGCCACCATGCCCAGCTAATTTTTTTT	TMPS*FFFFFXXKGXXXXX
				NNNAAAAAGGGNNTTNNTTNTNTNGCCCNGGNNGGTNTNAANCTCNTNNC	PXXVXXSXPXGIXPPXPPX
			_	CTNANGGNATTNNCCCNCCTNGNCCNCCAAANGGGCNGGANTT	GXX
Shidella	ဗ	prey14400	92	GGGCGAGAGGACTGAGTGTGCTGAGCCCCCCGGGACGAACCCCCGGGCTG 296	GERTECAEPPRDEPPADG
ospC1				ATGGAGCTCTGAAGCGGGCAGAGGAGCTCAAGACTCAGGCCAATGACTACT	ALNHAEELNI GAINDI FRAN
				TCAAAGCCAAGGACTACGAGAACGCCATCAAGTTCTACAGCCAGGCCATCG	DYEINAINT TOCATEDIATE
				AGCTGAACCCCAGCAATGCCATCTACTATGGCAACCGCAGCCTGGCCTACC	IYYGNESLAYLEI ECYGTA
				TGCGCACTGAGTGCTATGGCTACGCGCTGGGAGACGCCACGCGGGCCAII	LGUAI RAIELDANTINGTTA
				GAGCTGGACAAGAAGTACATCAAGGGTTATTACCGCCGGGCTGCCAGCAAC	HAASNMALGKFHAALHUTE
				ATGGCACTGGGCAAGTTCCGGGCCGCGCTGCGAGACTACGAGACGGTGGT	CNIKIVKOKAFFBAIAGOFH
				CAAGGTGAAGCCCCATGACAAGGATGCCAAAATGAAATACCAGGAGTGCAA	ONLY IN COLOR IN COLO

ACCEPANT CALLER

			000000000000000000000000000000000000000	SVEGET PIECES
			CAAGATCGTGAAGCAGAAGGCCTTTGAGCGGGCCATCGCGGGCGACGAGC	KHSVVDSLDIESMITIEDETS
			ACAAGCGCICCGIGGACTTGAAGACGCGAAAGAGACATCAAGACATCAAGTTCAT	WYKDQKKLHRKCAYQILVQ
			PARAGE AGE TO A TECHNOLOGIC AGE	VKEVLSKLSTLVETTLKETE
			TOCTACCAGATTCTGGTACAGGTCAAAGAGGTCCTCTCCAAGCTGAGGCACG	<itvcgdthgqfydllnife p="" <=""></itvcgdthgqfydllnife>
				NGLPSETNPYIFNGDFVD
				RGSFSVEVILTLFGFKLLYP
			CTCGGAGACCAACCCCTATATTTAATGGTGACTTTGTGGACCGAGGCTCC	DHFHLLRGNHETDNMNQIY
			TTCTCTGTAGAAGTGATCCTCACCCTTTTCGGCTTCAAGCTCCTGTACCCAGA	GFEGEVKAKYTAQMYELFS
			TCACTTTCACCTCCTTCGAGGCAACCACGAGACAGACATGAACCAGATC	EVFEWLPLAQCINGKVLIM
			TACGGTTTCGAGGGTGAGGTGAAGGCCAAGTACACAGCCCAGATGTACGAG	HGGLFSEDGVTLDDIRKIER
			CTCTTTAGCGAGGTGTTCGAGTGGCTCCCGTTGGCCCAGTGCATCAACGGC	NRQPPDSGPMCDLLWSDP
			AAAGTGCTGATCATGCACGGAGGCCTGTTCAGTGAAGACGGTGTCACCCTG	QPQNGRSISKRGVSCQFG
			GATGACATCCGGAAAATTGAGCGGAATCGACAACCCCCAGATTCAGGGCCC	PDVTKAFLEENNLDYIIRSH
			ATGTGTGACCTGCTCTGGTCAGATCCACAGCCACAGAACGGGCGCTCGATC	EVKAEGYEVAHGGHCVIV
			AGCAAGCGGGGCGTGAGCTGTCAGTTTGGGCCTGACGTCACCAAGGCCTTC	FSAPNYCDQMGNKASYIHL
			TTGGAAGAGAACAACCTGGACTATATCATCCGCAGCCACGAAGTCAAGGCC	QGSDLRPQFHQFTAVPHP
			GAGGGCTACGAGGTGGCTCACGGAGGCCGCTGTGTCACCGTCTTCTCTGCC	NVKPMAYANTLLQLGMM*
			CCCAACTACTGCGACCAGATGGGGAACAAAGCCTCCTACATCCACCTCCAG	
		_	GGCTCTGACCTACGGCCTCAGTTCCACGGTTCACAGCAGTGCCTCATCCCA	
			ACGTCAAGCCCATGGCCTATGCCAACACGCTGCTGCAGCTAGGAATGATGT	
Shigella 3	prev50029	96	CTCACCTCTGAAATTCCACAGCTCAATGACTGGAGGCTCTCTCCCACCCA	LISEIPOLNOWRLSPIHSH
ospC1			CAAGACATTGCCAGGAACGTCTTAAGACCTCAGGAGACCACTTCTTTAGTAA	HCCERCA SGUALFONGEL
			GCAATTTTTAGATGGATTCTCACTCTGTCACTCAGGCTGGAGTGCAGTGGC	HWILI LSLALECSGAVSAN
			GOGGICTCTGCTCACTACACCCTCCCTCCTGGCTCCTGCCCGTATGTAT	YTLPLLAPAHMYFSFSPCLL
			TCTCCTTCTCTCCATGCCTGCTCTGTAGGGACCATAGCCTCTGTCCCTGCAT	CRUHSLCPCIHVGHQSHQ
			ACATGTTGGACATCAATCACATCAGTCCACCAAGTAACTTCATCAAGCACCCA	SIK-LHGAPMYAGHSVPRV
			TGTACGCCCAGCACAGCGTCCCAAGGGTGCCCCACTTACCCACAGAAGAAG	PHLPTEERQLW'EI'LLAP
			AAAGGCAACTTTGGTAAGAGATCTGACTTCTAGCTCCAGTTCTGTCTAGC	VESLANVHOI HERAVF LEN
		_	AACGTGAGATGCACCCGGTTGAGGGCTGTTTTTTAATTGTTGAAAATGAAGG	MKD-I-MVCLKCFKMI-FYL
			ACTGAACTTAGATGGTCCAACTGAAATGTTTTAAAATGATATGATTGTACCLLA	KKHMKF-YIHNI GNF-KRYA
			AAAAGAGAAATGAAATTCTGATATATTCACAACACAGGAAACCCIIGAAAACGI	K-INKGDIMKGGITDSI TVIMS
			TATGCTAAATGAAATAAGGGAGACATGAAAGGACAAATATATGACTCCACTTA	LK*TTT*ROKVDSGC*GLLE
			TGTGATGTCCCTCAAATAGACAACCACATAGAGACAGAAAG I AGACAG I GGG	GCWHVSV-WVCCHSGCSV
		_	TGCTAGGGGTTGCTGGAGGGGCAATGGAGAGTTAGTGTTTAATGGGTACAG	YGVGILGSLYFSINNLADI
			TGTCACAGTGGCTGCTCTGTCTATGGAGTAGGCACTCTTGGGTCTCTTTACT	KEKALEIU
		-	COTOTTOTTO A COCCO A TOCA CA A COCCA TO A COCCO CA TAGGA CA A COCCA A CA C	AVI RGDAEAVKGIGSGKVL
Shigella 4	prey67563	76	GCIGIGIIGAGAGGCGAIGCAGAAGCAGICAACCACACIACCACACACA	

TODIESTRY DILITOR

Coci				GTCCTGAAGAGTGGCCCCCAGGATCACGTGTTCATTTACTTCACTGACCATG	KSGPQDHVFIYFTDHGSTG
da d				GATCTACTGGAATACTGGTTTTTCCCAATGAAGATCTTCATGTAAAGGACCTG	LVFPNEDLHVKDLNETIHY
				AATGAGACCATCCATTACATGTACAAACACAAAATGTACCGAAAGATGGTGTT	MYKHKMYRKMVFYIEACES
				CTACATTGAAGCCTGTGAGTCTGGGTCCATGATGAACCACCTGCCGGATAAC	GSMMNHLPDNINVYATTAA
				ATCAATGTTTATGCAACTACTGCTGCCAACCCCAGAGAGTCGTCCTACGCCT	NPRESSYACYYDEKRSTYL
				CTTACTATE ATE A CAGAGA COLONIA COLOR	GDWYSVNWMEDSDVEDLT
				ACTOCATOCATOCATOCATOCATOCATOCATOCATOCATO	KETLHKQYHLVKSHTNTSH
				A SOCIAL DESCRIPTION OF THE SECOND AND THE SECOND A	VMQYGNKTISTMKVMQFQ
				TEGAAACAAAACAAATCTCCACCATGAAGTGATGCAGTTTCAGGGTATGAAA	GMKRKASSPVPLPPVTHLD
				COCA A A GOOD A GENERAL TO TO COCATO	LTPSPDVPLTIMKRKLMNT
				COCCAGOCCAGOCCACACACACACAAAAAAAAAAAAAAA	NDLEESROLTEEIQRHLDA
				CAATGATCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RHLIEKSVRKIVSLLAASEA
				GEATGCCAGGCACCTCATTGAGAAGTCAGTGCGTAAGATCGTCCTTGCTG	EVEQLLSERAPLTGHSCYP
				ACAPACATION CONTRABATION OF THE TOTAL OF THE	EALLHFRTHCFNWHSPTYE
			_	CANCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	YALRHLYVLVNLCEKPYPL
				CTTCAACTGGCACTCCCCCACGTACGAGTATGCGTTGAGACATTTGTACGTG	HRIKLSMDHVCLGHY*
				CTGGTCAACCTTTGTGAGAAGCCGTATCCACTTCACAGGATAAAATTGTCCAT	
			_	CONTROL TO THE TOTAL THE T	
	,	0010101	a	GGACCACATIACTTTAGGATACTGCAAAATCTCAGCATTGGCTCTTC 299	TKDHHYFKYCKISALALLKM
Snigella	4	pieyzios	2	TARABATEGE SATE CATE CATE CAGA TO GA GA GA TITI GA A GA GA GA GA TO CA A TITI GA A GA TO GA TO CA A TITI GA A CA A TITI GA A GA TO CA A TITI GA A CA A TITI GA A CA A TITI GA A GA TO CA A TITI GA A CA A TITI GA A TITI	VMHARSGGNLEVMGLMLG
Ipan				TEATECTAGGAAAGGTGGATGGTGAAACCATGATCATTATGGACAGTTTTGC	KVDGETMIIMDSFALPVEGT
				TTTCCTGTGGAGGCACTGAAACCCGAGTAAATGCTCAGGCTGCTGATAT	ETRVNAQAAAYEYMAAYIE
				CAATACATGCTGCATACATAGAAAATGCAAAACAGGTTGGCCGCCTTGAAA	NAKQVGRLENAIGWYHSH
				ATECA ATCOCCTOCTATO AT AGO CACOCT GO CT ATGO CT GCT GCT GCT GG GCT T CT GG	PGYGCWLSGIDVSTQMLN
				A TTEATTATATACTACTCAGATGCTCAATCAGCAGTTCCAGGAACCATTTGTAG	QQFQEPFVAVVIDPTRTISA
				CALLICATION TO A TOTAL	GKVNLGAFRTYPKGYKPPD
				CAGE INCLUDE TO A TAKE TO A TAKE THE TOTAL TO A TAKE THE	EGPSEYQTIPLNKIEDFGVH
				CGCCIIIAGGACAIATOOACTTAATAAAAAAAAAAAAAAAAAAAATTTTGGTGTACACTGCAA	CKOYYALEVSYFKSSLDRK
			_	GAGIACCAGACIAIICCACIIAAIAAAAIAGAAAGAIIIIGGGGAAATTI	I FI WNKYWVNTLSSSSL
				ACAALALIAIGCOLIAGAAGICIOARALIOTOONAATAOOTOTTOAGATTOTTOTAGGT	I TNADYTTGOVEDI SEKLE
				GCTTGAGCTGTTGTGGGAATAACCACTGGGAATAGCTCTTTGATTTGTCTGAAAAGG	OSEAOLGRGSFMLGLETH
				TGCTTACTACTACTACTACTACTACTACTACTACTACTACTA	DRKSEDKLAKATRDSCKTT
				DANA COCATGA COGA A A A TOA GA A A A COTA A A A GO CA A A A GA A CA A A A A CA A A A A CA A A A	IEAIHGLMSQVIKDKLFNQIN
				GCTGTAAAAGTACCATAGAAGCTATCCATGGATTGATGTCTCAGGTTATTAAG	IS*
			_	GATABACTGTTTAATCAAATTAACATCTCTTAA	
		20130	8	GARCANTA A GARCAT GARGA CONTRACT CONTRACT CONTRACT SOU	GNKACSPCSSQSSSSGICT
Snigella	4	preyzoroo	60	TTOCACAGACTTCTGGGACTTATTGGTAAAACTGGACAACATGAATGTCAGC	DFWDLLVKLDNMNVSRKG
pan				CORRADAGE CARACTEC GTG A GT CAGT G C C C G G G G G G G G G G G G G G G	KNSVKSVPVSAGGEGETS
				GGGGGAAACCTCTCCATACAGCCTCGAGGCCTCTCCCACTGGGGCAGCTCAT	PYSLEASPLGQLMNMLSHP

HLADGPFAVLVDYIRVLDFD GEEGODAGGLLREWYMIIS MESEDYHFYQGLVYLLEND FDAANVLLOLSRGDSGTRD KI KGKMOSRFDMAENVVIV FI.PLLSEQUSUDELWDMLG VKRKYFRQELERLDEGLRK EDMAVHVRRDHVFEDSYR VSTLGYDLTFSTEVQEFGV VIRRSSLLTEKLLRLLSLISIA PTPPTAPTPVTSAPALVAAT AGCETLSPDGLPEEGPGTT EAEADAIIQMVREGQRARR SIASDGTPQGEKEKEERPP ECLKELEESHDQHAVLVLQ REMENPMYALFRISPGDR QLRDDTRRANKKAKQTGR QQQAATSESSQSEASVRR EESPMDVDQPSPSAQDTQ PAVEAFFI VHATERESKPP SPAPLTPATPSSLDPFFSR ELHRKSPEEMKNRLYIVFE VTYTINPSSHCNPNHLSYF **KFVGRIVAKAVYDNRLLEC** YFTRSFYKHILGKSVRYTD STTTATSTTSTTTTAASTT AISTIVVAASTTVTTPTTATT **QIGTLLAELREYNLEQORR** ASOKBPLGGRELQLPSMS MI TSKTSTOKFFLRVLQVII GSSGI GSASSIOAAVROL VRDTRESQLAHIKDEPPPL **EPSSMHISSSLPPDTOKFL PENKVSEACIANSGSGAS** TVSISPTTKGSKSPAKVSD GGSSSTDFKMVSSGLTEN QLQLSVEVLTSHSCSEEGL **TVLKLLLNGARHLGYTLCK** RFAETHRTVLNQILRQSTT TCGAGAGATGTTTAACCCTATGTATGCCTTGTTCCGTACCTCACCTGGTGATC GGACCAGCCATCTCCCAGTGCTCAAGATACTCAATCCATTGCCTCCGATGGA CCTCCTGTCCGAGACACCCGTGAGAGCCAGCTGGCACACATCAAGGACGAG CCTCCTCCACTCTCCCCTGCCCCCTTAACCCCCAGCCACGCCTTCCTCCTTG CCCTGACACACAGAAGTTCCTTCGCTTTGCAGAGACTCACCGCACTGTGTTA AACCAGATCCTACGGCAGTCCACGACCCACCTTGCTGATGGGCCTTTTGCTG TCCTGGTAGACTACATTCGTGTCCTCGACTTTGATGTCAAGCGCAAATATTTC CGCCAAGAGCTGGAGCGTTTAGATGAGGGGCTCCGGAAAGAAGAAGATGGCT GTGCATGTCCGTCGTGACCATGTGTTTGAAGACTCCTATCGTGAGCTGCATC AGAAGGGCAGGATGCTGGCGGGCTCCTGCGGGGAGTGGTATATGATCATCTC CACTOTTGTTCTGAGGAAGGCTTAGAGGATGCAGCCAACGTACTACTGCAGC TGAAGGGCAAAATGCAGAGCAGGTTTGACATGGCTGAGAATGTGGTAATTGT CAGGTCATCCAGCTCCGGGACGCGCGGGCCGGGCTAACAAGAAGCC GTCTAGCCAGTCAGAGGCGTCTGTCCGGAGGGAGGAATCACCCATGGATGT ACCCCACAGGGGGGAGAAAGGAAAGGAAAGACCACCTGAGTTACCCCTG CTCAGCGAGCAGCTGAGTTTGGACGAGCTGTGGGACATGCTTGGGGAGTGT CCTGCTGTCGAGGCCTTCTTCTGGTCCATGCCACAGAGCGGGAGAGCAAG GAGTCACCTACACCATCAATCCATCTTCCCACTGCAACCCCAACCACCTCAG CTCCTCAGACTCCTTTCTCTCATCTCAATTGCTCTCCCAGAAAACAAGGTGTC GGCTATTTCCACCATTGTCGTAGCTGCTTCGACCACAGTGACTACCCCCACG ACTGCTACCACTACTGTTTCAATTTCTCCCACTACTAAGGGCAGCAAATCTCC AGCGAAGGTGAGTGATGGGGGCAGCAGCAGTACAGACTTTAAGATGGTGTC CTCTGGCCTCACTGAAACCAGCTACAGCTCTCTGTAGAGGTGTTGACATCC TCTCCCGGGGGGGACTCTGGGACCCGGGACACTGTTCTCAAGCTGCTACTGA CAGGCAGCTGTTCGGCAGCTGGAGGCTGAGGCTGATGCCATTATACAAATG A C C C A T T T T T C C C G G G G C C C C C T T T G C A C C T C T C C T C A G C C T G C C GCAAATCCCCCGAAGAAATGAAGAATCGATTGTATATAGTATTTGAAGGAGA SAACATGTTGTCACACCCAGTCATCCGCCGGAGCTCTCTTAACTGAGAAA ATGGAGCCCGCCATCTGGGTTATACCCTTTGTAAACAAATAGGTACCCTGCT AAACCCTCTCCTGATGGCCTGCCTGAGGAGCAGCCACAGACCACGAGG GGCATCTCAGAAGCGACCTTTGGGTGGCCGGGGAGCTCCAGCTGCCTTCTAT GTCCATGTTGACATCCAAGACATCTACCCAGAAGTTCTTGAGGGTACTA AAGCAGACAGGCAGGCTAGGTTCCTCCGGTTTAGGCTCAGCTAGCAGCATC GTACGTGAGGGTCAAAGGGCGCGGAGACAGCAACAAGCAGCAACGTCGGA CTAAAGGAACTAGAGGAATCCCATGACCAGCATGCGGTGCTAGTGCTACAG AGAAGCACAGGCTAATTCTGGCAGCGGTGCTTCCTCCACCACCACTGCCAC CCCTACTGCACCCACCCCTGTCACTTCTGCTCCAGCCCTGGTTGCTGCCCAC CTCAACCACATCTACCACCACCACTGCCGCCTCCACCACGCCCACACC

IDDHEHBY DIIILDE

			CTACTTCAAGTTTGTCGGACGCATTGTGGCCCAAAGCTGTATATGACAACCGT	CEVRDLKPNGANILVTEEN
			CTTCTGGAGTGCTACTTTACTCGATCCTTTTACAAACACACATCTTGGGCAAGTC	KKEYVHLVCQMRMTGAIRK QLAAFLEGFYEIIPKRLISIFT
			GTTTATCTGCTGGAAAATGATGTCTCCACACTAGGCTATGACCTCACCTTCAG	EQELELLISGLPTIDIDDLKS
			CACTGAGGTCCAAGAGTTTGGAGTTTGTGAAGTTCG1GACC1CAAACCCAA1	ALRSFDQADRAKFLQFVTG
			GTATGCCAGATGAGAATGACAGGAGCCATCCGCAAGCAGTTGGCGGGCTTTC	TSKVPLQGFAALEGMNGIQ
			TTAGAAGGCTTCTATGAGATCATTCCAAAGCGCCTCATTTCCATCTTCACTGA	KFQIHRDDRSTDRLPSAHI
			GCAGGAGTTAGAGCTGCTTATATCAGGACTGCCCACCATTGACATCGATGAT	CENCILDIPAYESFERSATO
			CTGAAATCCAACACTGAATACCACAAGTACCAGTCCAACTCTATTCAATCAA	PNSVGFFLPLLDLGRGEL
			CTCCAGTTTGTCACGGGTACTTCCAAGGTACCCCTGCAAGGCTTTGCTGCCC	KKEPERNCOKPINEIHOLTV
			TCGAAGGCATGAATGGCATTCAGAAGTTTCAGATCCATCGAGATGACAGGTC	CVPAAPSSPAHICSSSHSL
			CACAGATOGCCTGCCTTCAGCTCACAIGIIIIAAICAGCIGGAICIGCCI	CVLKRO*
			GCCIAIGAGAGCIIIGAGAAGIICGGCCAATAAGGCCCTGCCCAACTCCGTGG	í
			GGTTTTTTTACCATTGTTGGACCTGGGGAGGGGGGGGTTAAAAAAAA	
			AGAAAGAAATTGTCAAAAAACCAATAAATGAAATCCACCAACTCACCGTGTGTG	
			TCCCAGCTGCCCCATCTTCCCCAGCGCATACCTGTTCCTCTTCTCTCTC	
			CCCGCCGCCTTTTCCTCACCTTCTCCCCTTTCCAIGCCGICCAIGAICC	
				THE COURT AND DELIVED
Shigella 4	prey53990	100	CCACCTATACCCCGGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGGGGGGGG	I Y I PGDCFNFAAFRREVAF
			TGGCACCACCCTATCAGGGGGCTGACCCCA CCI GCGACAGCCC CCC	P TOGADFICATACASDI IFIN
			CCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACAGC	PLUKWEDSAHRFUSLUID
			CACAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGA	DPAIL YAVENVPPLRWNE
			ACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGG	FVRRLGLSUHEIURLELGIN
			GACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGC	GRCCREACTS MICAL WHICH
			GGCGCAATACAGCATGCTGGCGACCTGGAGCGGCGCGCACACGCGGCGCGCGC	I GCI ENIFEAI CGPAAI PP
			GAGGCCACGCIGGAGCIGCIGGAGCCCGIGCICCGCGACAIGGCGCACAIGGCGCCCACAIGGCGCCCCCCCC	APSI I B*
			GGGC GCC GGAGGACAT CAAGAAGCGCTTTCCCCCCCCCC	
Shigella 4	prey9120	101	GCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCATGCCCGGGGGTGCG 302	ATRSSAVRLRSSVPGVRLL
			GCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCACGCCATCAACGCAA	RTNEKVELGELNDRFANYI
			CONTROL OF TACATOR OF	DKVRFLEGONKILLAELEGL
			GATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCC	KGGGKSRLGDLYEEEMRE
			TAGGGGACCTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGCAGGTGGAC	LRRQVDQLTNDKARVEVE
			CAGCTAACCAACACAAAGCCCGCGTCGAGGTGGAGCGCGCGACAACCTGGC	RDNLAEDIMHLHEKLQEEM
			CGAGGACATCA I GCGCC I CCGGGAGAAA I IGCAGGAGAGAI GC I I CAGAG	רמורבאבוורמטווימ

INDARAFAY DILLIB

				AGAGGAAGCGAAAACACCTGCAATCTTTCAGACAGGATGTTGACAATGCG TCTCTGGCACGTCTTGACCTTGAACGCAAAGTGGAATCTTTGCAAGAAGAGA	NASLARLDLERKVESLOEEI AFLKKLHEEEIQELQAQIQE
				TTGCCTTTTTGAAGAAACTCCACGAAGAGAAATCCAGGAGCTGCAGGCTCA	QHVQIDVDVSKPDLI AALH
				GATTCAGGAACAGCA GI CCAAA I CGA I GI I GGA I GI I I CCAAGCCI GACCI C	EWYKSKFADLSEANRIN
				ACCIGO GOOGLO CONTROLLO CO	DALRQAKQESTEYRRQVQ
				AGGCTGCCAACCGGAACAATGACGCCCTGCGCCAGGCAAAGCAGGAGTCC	SLTCEVDALKGTNESLERQ
				ACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCTT	MREMEENFAVEAANYQDTI
				AAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAAC	GRLODEIONMKEEMARHL
				TTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGCCGCCTGCAGGATG	REYQDLLNVKMALDIEIATY
				AGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAAGA	RKLLEGEESHISLPLPNFSS
				CCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCIACAGGAAG	DIE INTIVETBRECOVINETS
				CTGCTGGAAGGCGAGGAGGAGGATTTCICIGCCICIICCAAACIIIICCI	אווייים ואוויים
				COCTGAACCTGAAGGAAACTAATCIGGAIICACICCICLIGGIIGAIACCCA	
				CTCAAAAAGGACATTCCTGATTAAGACGG	
Chicollo		prev67571	100		PXYGDXXXGPXWKDHLMX
					RCKF-CXRSGQXPXLCXSX
, yan				TTTCCNCAGGCTGGCAGTGGTGANGATGCTGCGGTCCAGGCAGGGAGCTG	GWQW*XCCGPGRELLLQG
				CTTTGCAGGGTGAGGCGGTGGANGGCTGCAACACNCCCCNGACCCCNTCT	EAVXGCNTPXTPSPFSNAX
				CCNTTCTCAAATGCTGNGANGACTGGAATNNTCCATAGANNANGTTTCTTTT	XTGXXHRXXFFFXXXXXE
				_	
Shinella		prev67572	103	TCCTTTNAGGATGNTGAAAAGANGAATATATGCTTGGGAGCATGNNGTATCT 304	SFXDXEKXNICLGAXXIFXV
Cedi				TTNTGGTAGCATNACGCCATGNCCTACTTGTGCTTNNNNCACTTNGTTTNNN	AXRHXLLVLXXLXXXGLQH
) Jack				NGGACTACAACATGGAGGAANTNNACCNNATCTACCCTNTAGGCCTGCTCNT	GGXXPXLPXRPAXGLLXVS
				GGTCTCCTTGNTGTATCATGCCCTCGCTGGTNTGGAGCCNNNGCGGGNCCT	CPRWXGAXAGPLXYASXIP
				CTTGANTATGCTTCANCCATACCAACACTGGTTGTATGTACGCGATCGCAAC	TLVVCTRSQHXMHVCXLLY
				ATCANATGCACGTATGTTNCTTGCTGTACAGACGCTACNAGAGANGGGCTTC	RRYXHXASLX
				CCTGNATN	VAATHUTTUNGVGDEESV
ella	4	prey65696	104	TGCTGCTGCCACCACCACCACCACTGATAATGGTGTGTGGGGTCCTGGATGAAGAAATGATGAAGAATTCATGAATTCATGAGAATGAGAATGAAT	DPNOYYKIRSQAIHQLKVN
IbaD				CTGAAGGTCAATGGGGAAGACCCATACCCACACACACATCCATGTAGACATCT	GEDPYPHKFHVDISLTDFIQ
				CACTCACTGACTTCATCCAAAAATATAGTCACCTGCAGCCTGGGGATCACCT	KYSHLQPGDHLTDITLKVA
				GACTGACATCACCTTAAAGGTGGCAGGTAGGATCCATGCCAAAAGAGCTTCT	GRIHAKRASGGKLIFYDLR
				GGGGGAAAGCTCATCTTCTATGATCTTCGAGGAGAGGGGGGTGAAGTTGCAA	GEGVKLQVMANSRNYKSE
				GTCATGGCCAATTCCAGAAATTATAAATCAGAAGAAGAATTTATTCATATTAAT	EEFIHINNKLANGUIIGVQG
				AACAAACTGCGTCGGGGAGACATAATTGGAGTTCAGGGGAATCCTGGTAAAA	NPGKTKKGELSIIPYEITLLS
				CCAAGAAGGGTGAGCTGAGCATCATTCCGTATGAGATCACACTGCTGTCTCC	VECHMILPHICHFGLNDNEIN
				CIGILIGCALAIGILACCICALCILOACILIGAGACAAAGACAAGACAAA	

INCHESANT DILITOR

				GGTATCGCCAGAGATACTTGGACTTGATCCTGAATGACTTTGTGAGGCAGAA ATTATCATCCGCTCTAAGATCATCACATATATAAGAAGTTTCTTAGATGATGAGCT	ш <u>г</u>	RSKIITYIRSFLDELGFLEIET PMMNIIPGGAVAKPFITYHN
				GGGATTCCTAGAGATTGAAACTCCCATGATGAACATCCTAGGGGGGGG	ш 5	ELDMNLYMRIAPELYHKML
				CGTGGCCAAGCCTTTCATCACTTATCACAAGGGGGGGACAIGAACIIAIAIA	> 0	DLTHNPEFTTCEFYMAYAD
				GAGAAI GC CCAGAAC CA CA CA CA CA	>	YHDLMEITEKMVSGMVKHI
				CACAATCCTGAGTTCACCACCTGTGAGTTCTACATGGCCTATGCAGACTATC	⊢ (TGSYKVTYHPDGPEGQAY
				ACGATCTCATGGAAATCACGGAGAAGGTTTCAGGGATGGTGAAGCAIAI	7 4	DVDFI PPFFFFININIVEELER
				TACAGGCAGTTACAAGG	(DDICVAKAVECPPPRTTA
				CTTGAGAAAGCCCTGGGGATGAAGCTGCCAGAAAGGAACCTCTTTGAAACTG	Œ	RLLDKLVGEFLEVTCINPTFI
				AAGAAACTCGCAAAATTCTTGATGATATCTGTGTGGCAAAAGCTGTTGAATGC	<u> </u>	CDHPQIMSPLAKWHRSKE
				CCTCCACCTCGGACCACGCCAGGCTCCTTGACAAGCT1G1TGGGGAG11C	ם כ	GLIERFELTVINNEIGIATI
				CTGGAAGTGACTTGCATCAATCCTACAITCAICIGIGAICACCCACAGAIAAI	א ה	KAAGDDEAMEIDENECTAI
				GAGCCCTTTGGCTAAA1GGCACCGCICIAAAGAGGGICIGAACIGAAGGGGIII	: 11	FYGI PPTAGWGMGIDRVA
				GAGCIGITIGICALGAAGAAGAGAGATTTTTGAAGAACAGGCCAAGGCCAAGGCTG	2	MFLTDSNNIKEVLLFPAMKP
				CAGGTGATGATGAGGCCATGTTCATAGATGAAAACTTCTGTACTGCCCTGGA	Ш	EDKKENVATTDTLESTTVG
				ATATGGGCTGCCCCCACAGCTGGCTGGGCATGGGCATTGATCGAGTCGC	_	-SV*
				CATGTTTCTCACGGACTCCAACAACATCAAGGAAGTACTTCTGTTTCCTGCCA		
				TGAAACCCGAAGACAAGAAGGAGAATGTAGCAACCACTGATACACTGGAAAG		
						ALL COLORS
Shinella	4	prev8889	55	GCTCAAGCCGGAGTTCATGCGGCGGCCGGACAAGTCCTTCGACCCCTTCAC 306		LKPEFMHHPDKSFDFFIEV
all Cleri	-			TGAGGTCATCGTGGATGGCATCGTGGCCAATGCCTTGCGGGTCAAGGTGAT	_ '	INDGIVANALHVKVISGUFL
3				CTCAGGGCAGTTCCTGTCCGACAGGAAGGTGGGCATCTACGTGGAGGTGGA	1 10	SDRKVGIYVEVDMFGLPVD
				CATGITTGGCCTCCCTGTTGATACGCGGCGCAAGTACCGCACCCGGACCTC	-	TRRKYRTRTSOGNSFNPV
				TCAGGGGAACTCGTTCAACCCCGTGTGGGACGAAGAGAGCCCTTCGACTTCCC	اح	WDEEPFDFFKVVLP1LASL
				CAAGGTGGTGCTGCCCACGCTGGCTTCACTTCGCATTGCAGCCTTTGAGGA	<u>- '</u>	RIAAFEEGGKFVGHRILFVS
				GGGGGGTAAATTCGTAGGGCACCGGATCCTGCCTGTCTCTGCCATCCGCTC	4 (AIRSGYHYVCLRINEANGFL
				CGGATACCACTACGTCTGCCTGCGGAACGAGGCCAACCAA	<u>, L</u>	CLFALLIY IEASD TIF DDRG
				GCCGGCCCTGCTCATCTACACCGAAGCCTCGGACTACAIICCIGACGACCA		OTAEALINFINAN SLINDGRA
				CCAGGACTATGCGGAGGCCCTGATCAACCCCCATTAAGCACGTCAGCCTGAT		HOLAALIGESEAGAGGETO
				GGACCAGAGGGCCCGGCAGCTGGCCGCCCTCATIGGGGAGAGIGAGGCIC	<u>, , , , , , , , , , , , , , , , , , , </u>	CDI COCCEGGGF SSINI II
				AGGCTGGCCAAGAGACGTGCCAGGACACCCAGICICAGCAGCIGGGGICI	, ,	TEL SEPERATION IASII SEV
				CAGCCGTCCTCAAACCCCCACCCCCACIGGAIGCCICCCCCCGCGG	_	APTEL DEL BGHKALVKLBS
				COCCCTGGCCCCACCACCTCCCTGCCAGCACCTCTCAGCAGCCCAGG		AF IFEDERING INSENIE IS
				GCAGCGTGATGATCTCATCGCCAGCATCCTCTCAGAGGTGGCCCCCCCC		TI TODI I DOI VOVOVEGED
				GCTGGATGAGCTCCGAGGTCACAAGGCTCTGGTCAAGCTCCGAAGGCAGC		RI BPGAI GGAADVEDTKE
				AAGAGCGAGACCIGCGGGAGCIGCGCAAGAAGCAICAGCGGAAGGAA	1	

TOOTSTRY DILLION

		ACCCTCACCCGCCGCCTGCTGGATGGCCTGGCTCAGGCACAGGCTGAGGG CAGGTGCCGGCTGCGGCCAGGTGCCCTAGGTGGGGGCCGCTGATGTGGAGG	<u>53</u>	GEDEAKRYQEFQNRQVQS LLELREAQVDAEAQRRLEH
		ACACGAAGGAGGGGACGACGAGGCAAAGCGGTATCAGGAGTTCCAGAAC	<u> </u>	LROALORLREVVLDANTTO EKRI KEMNEBEKKEI OKII
		GGCCCAGCGGAGGCTGGAACACCTGAGACAGGCTCTGCAGCGGCTCAGGG	<u> </u>	DRKRHNSISEAKMRDKHKK
		AGGTCGTCCTTGATGCAAACACAACTCAGTTCAAGAGGCTGAAAGAGATGAA	EA	EAELTEINRRHITESVNSIR
		CGAGAGGAGAAGAAGGAGCTGCAGAAGATCCTGGACAGAAAGCGCCATAA	귙	RLEEAQKQRHDRLVAGQQ
		CAGCATCTCGGAGGCCAAGATGAGGGACAAGCATAAGAAGGAGGCGGAACT	8	QVLQQLAEEEPKLLAQLAQ
		GACGGAGATTAACCGTCGGCACATCACTGAGTCAGTCAACTCCATCCGTCG	낊	ECQEQRARLPQEIRRSLLG
		GCTGGAGGAGGCCCAGAAGCAGCGGCATGACCGTCTTGTGGCTGGGCAGC	2	EMPEGLGDGPLVACASNG
		AGCAGGTCCTGCAACAGCTGGCAGAAGAGGAGCCCAAGCTGCTGGCCCAG	¥i	HAPGSSGHLSGADSESQE
		CTGGCCCAGGAGTGTCAGGAGCAGCGGGCGAGGCTCCCCCAGGAGATCCG	<u> </u>	ENIOL.
		GTGGCCTGTGCCAGCAACGGTCACGCACCCGGGAGCAGCGGGCACCTGTC		
		GGGCGCTGACTCGGAGAGCCAGGAGAACACGCAGCTCTGA		
prey700	9	-	_	MGIGLSAQGVNMNRLPGW
		GGGATAAGCATTCATATGGTTACCATGGGGATGATGGACATTCGTTTTGTTCT	ž	DKHSYGYHGDDGHSFCSS
		TCTGGAACTGGACAACCTTATGGACCAACTTTCACTACTGGTGATGTCATTG	<u>15</u>	GTGQPYGPTFTTGDVIGCC
		GCTGTTGTGTTAATCTTATCAACAATACCTGCTTTTACACCAAGAATGGACAT	Z I	VNLINNTCFYTKNGHSLGIA
		AGTTTAGGTATTGCTTTCACTGACCTACCGCCAAATTTGTATCCTACTGTGGG	E :	FTDLPPNLYPTVGLQTPGE
		GCTTCAAACACCCAGGAGAAGTGGICGATGCCAATITTGGGCAACAICCIIIC	> 1	VVDANFGQHPFVFDIEDYM
		GIGTTIGATATAGAAGACIAIATGCGGGAGIGGAGAACCAAAAICCAGGCAC	# 6	REWRINGACIDHEPIGDH
		ACABABABATGGTTTCATCTTATTTAGTCCACCATGGGTACTGTGCCACGCAG	3 9	HGYCATAEAFARSTDOTVL
		AGGCCTTTGCCAGATCTACAGACCAGACCGTTCTAGAAGAATTAGCTTCCAT	Ш	EELASIKNRORIOKLVLAGR
		TAAGAATAGACAAAGAATTCAGAAATTGGTATTAGCAGGAAGAATGGGAGAA	W	MGEAIETTQQLYPSLLERN
		GCCATTGAAACAACACAGTTATACCCAAGTTTACTTGAAAGAAA	<u>R</u>	PNLLFTLKVRQFIEMVNGT
		TCTCCTTTTCACATTAAAAGTGCGTCAGTTTATAGAAATGGTGAATGGTACAG	SO	DSEVRCLGGRSPKSQDSY
		ATAGTGAAGTACGATGTTTGGGAGGCCGAAGTCCAAAGTCTCAAGACAGTTA	≧	PVSPRPFSSPSMSPSHGM
		TCCTGTTAGTCCTCGACCTTTTAGTAGTCCAAGTATGAGCCCCAGCCATGGA	壴	NIHNLASGKGSTAHFSGFE
		ATGAATATCCACAATTTAGCATCAGGCAAAGGAAGCACCGCACATTTTCAG	၁	SCSNGVISNKAHQSYCHSN
		GTTTTGAAAGTTGTAGTAATGGTGTAATATCAAATAAAGCACATCAATCA	Ξ	KHQSSNLNVPELNSINMSR
		GCCATAGTAATAAACACCAGTCATCCAACTTGAATGTACCAGAACTAAACAGT	S	SQQVNNFTSNDVDMETDH
		ATAAATATGTCAAGATCACAGCAAGTTAATAACTTCACCAGTAATGATGTAGA	X.	YSNGVGETSSNGFLNGSS
		CATGGAAACAGATCACTACTCCAATGGAGTTGGAGAAACTTCATCCAATGGT	<u>주</u>	KHDHEMEDCDTEMEVDSS
		TTCCTAAATGGTAGCTCTAAACATGACCACGAAATGGAAGATTGTGACACCG	정	QLRRQLCGGSQAAIERMIH
		AAATGGAAGTTGATTCAAGTCAGTTGAGACGCCAGTTGTGTGGGAGGAAGTCA	2	FGRELQAMSEQLRRDCGK
		GGCCGCCATAGAAAGAATGATCCACTTTGGACGAGAGCTGCAAGCAA	볼	NTANKKMLKDAFSLLAYSD
		TGAACAGCTAAGGAGAGACTGTGGCAAGAACACTGCAAACAAA	M	PWNSPVGNQLDPIQREPV

IDENIHEZ DIZIEE

			AAGGATGCATTCAGTCTACTAGCATATTCAGATCCCTGGAACAGCCCAGTTG	CSALNSAILETHNLPKQPPL ALAMGQATQCLGLMARSGI
		, < <u>-</u>	TGGAATATTAGAAACCCACAATCTGCCAAAGCAACCTCCACTTGCCTAGGA TGGGAAGAGGCACAATGTTGGACTGTGGTTGGATGATGGATG	GSCAFATVEDYLH*
prey2694	12	107	ATGGCACACGCTATGGAAAACTCCTGGACAATCAGTAAAGAGTACCATATTG 308	MAHAMENSWTISKEYHIDE EVGFALPNPOENLPDFYND
			TATAATGACTGGATGTTCATTGCTAAACATCTGCCTGATCTCATAGAGTCTGG	WMFIAKHLPDLIESGQLRE
			CCAGCTTCGAGAAAGAGTTGAGAAGTTAAACATGCTCAGCATTGATCATCTC	RVEKLNMLSIDHLTDHKSQ
		~	ACAGACCACAAAGTCACAGGCGCCTTGCACGTCTAGTTCTGGGATGCATCACCA	RLARLVLGCITMAYVWGKG
		, - (TGGCATATGTGTGGGGCAAAGGTCATGGAGATGTCCGTAAGGTCTTGCAA	SKKI FI PPII VYADCVI ANW
			GAAATATTGGTTTATGCAGACTGTGTCTTGGCAAACTGGAAAAAGGATCCTAA	KKKDPNKPLTYENMDVLFS
			TAAGCCCCTGACTTATGAGAACATGGACGTTTTGTTCTCATTTCGTGATGGAG	FRDGDCSKGFFLVSLLVEIA
		_	ACTGCAGTAAAGGATTCTTCCTGGTCTCTCTATTGGTGGAAATAGCAGCTGC	AASAIKVIPTVFKAMQMQE
		-	TTCTGCAATCAAAGTAATTCCTACTGTATTCAAGGCAATGCAAATGCAAGAAC	RDTLLKALLEIASCLEKALQ
			GGGACACTTTGCTAAAGGCGCTGTTGGAAATAGCTTCTTGCTTG	VEHQIHDHVNPKAFFSVLRI
			CCTTCAAGTGTTTCACCAAATCCACGATCATGTGAACCCAAAAGCATTTCA	YLSGWKGNPCLSDGLVYE
			GTGTTCTTCGCATATATTTGTCTGGCTGGAAGGCAACCCCCAGCTATCAGA	GFWEDPREFAGGSAGGSS
		_	CGGTCTGGGGTGTATGAAGGGGTTTCAGTGGTTTGAGGTGCTGGTGGTGGTGGTGGGTG	AAOFLODMBRYMPPAHBN
			CCAGCAGACTGCTGGTGGAGGACATGCTGCTCAGTTCCTCCAGGACATGAG	FLCSLESNPSVREFVLSKG
		_	AAGATATATGCCACCAGCTCACAGGAACTTCCTGTGCTCATTAGAGTCAAAT	DAGLREAYDACVKALVSLR
		_	CCCTCAGTCCGTGAGTTTGTCCTTTCAAAAGGTGATGCTGGCCTGCGGGAA	SYHLQIVTKYILIPASQQPKE
		_	GCTTATGACGCCTGTGTGAAAGCTCTGGTCTCCCTGAGGAGCTACCATCTGC	NKTSEDPSKLEAKGTGGTD
		_	AAATCGTGACTAAGTACATCCTGATTCCTGCAAGCCAGCGAAGGAGAAA	LMNFLKTVRSTTEKSLLKE
		_	TAAGACCTCTGAAGACCCTTCAAAACTGGAAGGCAAAGGAACTGGAACTGGAATTTAATAAATA	5
			GAAGGAAGGTTAA	
prey53735 108	۱ŏ		GGGTGAACCAGAAGGTTCCTTCGTGGATTACCAAACAACTATGGTGCGGACA 309	GEPEGSFVDYQTTMVRTA
			AGCCCAGAGAGCTGGGCCCTCTTGCTAACCAGCTGACCAGTGACTATGGC	ELGPLANQLTSDYGRLASE
			CGTCTGGCCTCGGAGGCCAAGCCTGCAGCGGTGGCTGCTGAAAATGAAGA	AKPAAVAAENEEIGSHIKHR
		_	GATAGGTTCCCATATCAAACACCGGGTACAGGAGCTGGGCCATGGCTGTGC	VQELGHGCAALVTKAGALQ
		_	CGCTCTGGTCACCAAGGCAGGCGCCCTGCAGTGCAGGCCCCAGTGATGCCTA	CSPSDAYTKKELIECARRV
		_	CACCAAGAAGGAGCTCATAGAGTGTGCCCGGAGAGTCTCIGAGAAGGICIC	SEKVSHVLAALQAGNAGI
			CCACGTCCTGGCTGCGCTCCAGGCTGGGAATCGTGGCACCCAGGCCTGCAT	MEATAGE! NBEGTETEADH
			ATGITTOGCACTGCTGGCACGCTCATCGTGAGGGTACTGAAACTTTCGCTG	REGILKTAKVLVEDTKVLVQ
	4	1		

			ľ	ACCACCGGGAGGGCATCCTGAAGACTGCGAAGGTGCTGGTGGAGGACACC	NAAGSQEKLAQAAQSSVA
			_	AAGGTCCTGGTGCAAAACGCAGCTGGGAGCCAGGAGAAGTTGGCGCAGGC	TITRLADVVKLGAASLGAED
				TGCCCAGTCCTCCGTGGCGACCATCACCCGCCTCGCTGATGTGGTCAAGCT	PETQVVLINAVKDVAKALG
				GGGTGCAGCCAGCCTGGGAGCTGAGACCCTGAGACCCAGGTGGTACTAA	DLISATKAAAGKVGDDPAV
				TCAACGCAGTGAAAGATGTAGCCAAAGCCCTGGGAGACCTCATCAGTGCAA	WQLKNSAKVMVTNVTSLLK
				CGAAGGCTGCAGCTGGCAAAGTTGGAGATGACCCTGCTGTGTGGCAGCTAA	TVKAVEDEATKGTRALEAT
				AGAACTCTGCCAAGGTGATGGTGACCAATGTGACATCATTGCTTAAGACAGT	TEHIRQELAVFCSPEPPAKT
				AAAAGCCGTGGAAGATGAGGCCACCAAAGGCACTCGGGGCCCTGGAGGCAA	STPEDFIRMTKGITMATAKA
				CCACAGAACACATACGGCAGGAGCTGGCGGTTTTCTGTTCCCCAGAGCCAC	VAAGNSCRQEDVIATANLS
				CTGCCAAGACCTCTACCCCAGAAGACTTCATCCGAATGACCAAGGGTATCAC	RRAIADMLRACKEAAYHPE
				CATGGCAACCGCCAAGGCCGTTGCTGCTGGCAATTCCTGTCGCCAGGAAGA	VAPDVRLRALHYGRECAN
				TGTCATTGCCACAGCCAATCTGAGCCGCCGTGCTATTGCAGATATGCTTCGG	GYLELLDHVLLTLQKPSPEL
				GCTTGCAAGGAAGCAGCTTACCACCCAGAAGTGGCCCCTGATGTGCGGCTT	KQQLTGHSKRVAGSVTELI
				CGAGCCCTGCACTATGGCCGGGAGTGTGCCAATGGCTACCTGGAACTGCTG	QAAEAMKGTEWVDPEDPT
				GACCATGTACTGCTGACCCTGCAGAAGCCAAGCCCAGAACTGAAGCAGCAG	VIAENELLGAAAAIEAAAKK
				TTGACAGGACATTCAAAGCGTGTGGCTGGTTCCGTCACTGAGCTCATCCAGG	LEGLKPRAKPKEADESLNF
				CTGCTGAAGCCATGAAGGGAACAGAATGGGTAGACCCAGAGGACCCCACAG	EEQILEAAKSIAAATSALVK
				TCATTGCTGAGAATGAGCTCCTGGGAGCTGCAGCCGCCATTGAGGCTGCAG	AASAAQRELVAQGKVGAIP
				CCAAAAAGCTAGAGCAGCTGAAGCCCCGGGCCAAACCCAAGGAGGCAGATG	ANALDDGQWSQGLISAAR
				AGTCCTTGAACTTTGAGGAGCAGATACTAGAAGCTGCCAAGTCCATTGCAGC	MVAAATNNLCEAANAAVQ
				AGCCACCAGTGCACTGGTAAAGGCTGCGTGGCTGCCCAGAGAGAACTAGT	GHASQEKLISSAKQVAAST
				GGCCCAAGGGAAGGTGGGTGCCATTCCAGCCAATGCACTGGACGATGGGC	AQLLVACKVKADQDSEAM
				AGTGGTCCCAGGGCCTCATTTCTGCTGCCCGGATGGTGGCTGCGGCCACCA	KRLQAAGNAVKRASDNLVK
				ACAATCTGTGTGAGGCAGCCAATGCAGCTGTACAAGGCCATGCCAGCCA	AAQKAAAFEEQENETVVVK
				AGAAGCTCATCTCATCAGCCAAGCAGGTAGCTGCCTCCACAGCCCAGCTCC	EKMVGGIAQIIAAQEEMLRK
				TTGTGGCCTGCAAGGTCAAGGCTGACCAGGACTCGGAGGCAATGAAACGAC	ERELEEARKKLAQIRQQQY
				TTCAGGCTGCTGCCAACGCAGTGAAGCGAGCCTCAGATAATCTGGTGAAAG	KFLPSELRDEH*
				CAGCACAGAAGGCTGCAGCCTTTGAAGAGCAGGAGAATGAGACAGTGGTGG	
				TGAAAGAGAAGATGGTTGGCGGCATTGCCCAGATCATCGCAGCACAGGAAG	
				AAATGCTTCGGAAGGAACGAGAGCTGGAAGAGGCGCGGAAGAAACTGGCC	
				CAGATCCGGCAGCAGCAGTACAAGTTTCTGCCTTCAGAGCTTCGAGATGAG	
				CACTAA	
Shigella	4	prey67574	109	NNACAGGAGANTGAGTTGCAANCGGCGGGTGATGCNNNTCTACCNGNNCGT 310	XQEXELQXAGDAXLPXRXR
ipaD				GNACGANCCACAGACGCCNCTNCCTGGGTCCTGGGGATNCCAAACNACANNN	XI DAXXW VLGXQI I XXXI X
				NCATNTACNTTNGTCTNTGTCAGANCANNCTGNGGNTGCACTNCNNNCGTCA	VXVRXXXGCTXXVIA*XXX
				TTGCTTAACNNNACNAGATGCCNCGTCATTTCNAGNCACNCATACAATACCA	MPRHFXXXIQYHXXX*FXFX
				CNTGCNTGNGTGATTTNTTTTTNGANNTGCCAATTNTGATGAAGGAACATA	XCQX**REHXXSWELVFLX
				TNTNTTCATGGGAATTGGTCTTTCTGTTNANNGTNTNAACAC	XVXT
Shigella	22	prey67509	110	110 GCTACTCACCCACCTCTCCCAGCTACTCGCCCACCTCTCCCAGCTATTCGCC 311	YSPTSPSYSPTSPSYSPTS

AGENTI L'ACCOAGUTINI TOUGANT IN TOUGANG TOUR CANDING AGENTI L'ACCOAGUTINE AGENT AGEN	CACCTCTCCCAGCTACTCACCCACTTCCCCTAGCTATTCGCCCACTTCCCCT AGCTACTCGCAAGGTCTCCCAGCTATTCGCCAGCTACTCGC AGCTACTCGCAGCTATTCCCAGCTATACTCCCAGCTATACTCTCCCAGCTATACTCTCCCAGCTATACTCTCTCCAGCTAACTCTCTCCCAGCTAACTCTCTCCCAGCTAACTCTCTCT
	AACTT GCTAT CACCA AGCTA
11. 1	CTACC
	ACC CA ACC CA
11. 1	CCAGTCTACAC CGCCCACTTCC CCCCAAAGG CCCCACCTACA GGAGAACTGA
11	TGCAC GACC TGGG TTGGG CACTC
CCCCCI GCAGCIAI I I CCCAAI GI GGAGGI I CCCCI I CI AI CI GCI GI G	TGG/ CAACA CCAACA CCAACA CCAACA CCTCA TGGI TAGI

ATCGT ACFGLPPWCYCCHSTTVP TGGTG RHKIPSIPRLA* TCCCA	CGCC 314 QDYOASQAEADQOQTRLK CGAG ELESQYSQELEKAELEREN SGGA ELOSQYSQUER TIGCA EALATAEOACKEKLHSLTQ GGAG AKEESKQLCLIEAOTMEA CCCA LIALLPELSVL	315	CTGG 316 XEXXMPGQGGIGXXWI'	ATOCT SUFFICE AT MYADD-PNELELLEKNU, DN SVFSEHRNLGANLLITARKA SOCTO DRITKMEN'INRLDNYOAPA DRITKMEN'INRLDNYOAPA SOTGA ASTTC DNYITSAVON'IETERAFIRE DNYITSAVON'IETERAFIRE ASTTC DNYITSAVON'IETERAFIRE DNYITSAVON'IETERAFIRE AGAGAA REFERENCYOARANTSGNW EELVKYLOMARKKARESYV STGTG EELVKYLOMARKKARESYV STGTG EELVKYLOMARKKARESYV	CCCG 318 AVGEISHLIEPLANAAPAEA TAGTT SQLGHKVSQNAQYFEPLTL AGCCA AAVGAASKTLSHPQQMALL FGTGC AGGNPKQAAHTQEALEEA AGGNPKQAAHTQEALEEA
GITTATGAAAAGAAAGATAATACATTICGTATGGCTATTICCATTCCAAATCGT ATCTTTCCAATAACAGCACCTTACACTGCTTGGTTTGGT	CCAGGACATOCAGGCCAGGCGAGGGTGACCAGCAGCAGCAGCATCGCC TCAAGGAGGTGAAGAGAGAGCATGAGAGTGAGCATCGAG TCAAGGAGGTGGAATCCAAGGTTGACAGATGAAGAGAAGAAGAGAGAG	GGCCGAGGAGAGAGAGACACACTGCAGGCCGAGTGTGACCAGTACCGCA 315 GCATCCTGGCGGAAAGAGGGAGGATGCTCAAAGACCTGCAAAAGAAGGTG GAGAGCGAGAGGGGGGGGGG	GANGAATNCNNTATGCCAAAAGGACAAGGAGGTATTGGTNGCTTANGCTGG CTATGAATACNTCNTTCGTTGTTGTAAANCTATTTGTTAGCACCNTCNGGCAT GGTAGGCAANGCCAAGTANATGCCAATCTATGAGGGCTGNNGGCAA GTTAGGCAANTGCAACTANATGCACAATCTATGAGGCTGNNGGCAGCAT TNCGATTANCTTANATGCATCTNGTTANNGGNTGNGGCCGNNCGGTTCC TNCCGATTNTGTTCNGGNAACAGCCTGGTGTNTGACANCTCGGACCGNN NACTATNACCTCCTGGAGGACCTACCACAGANGCATGCTGGTGGT ANGTANACCTCCTGGAGGACCTACCACAGANGCATGCTGGTGGGGAGGTGCAAGAGGGGGGTGTAACAGAGGGGGGGG	ONTGACTGCAGACCTTCCTAATGACTCATTGAACTGGGAGAAAAATGTC CTTGAATAGTCTGTTAATGACTCATTGAACTGGGAATACTGGAACAAGCTCCTTATCCT CATGAATAGTCTGTTTTAAGCTGAACAGGGAATCTGGAAAACCTCCTTATCCT CGAGAAACATTTAAGCTGACAGATGTTTATGGAGTATATTAACCGCCTTATCCT GGAAGAGCATTTGACCAATATGCCAAATATTGATGCAATACATTGAGCATTT GGAAGAGCATTTGAGCAATATTGAATGCTCAATACATTGAGCATT GGAAGCATTTGAAGCAACTTGGAAACTTGGAACATTGAATACATTGACGA ACGTTCAATTGAATGCTGCGAGTTGAATACATTGACAAACAGCAGTTGAAAAACAAGCAGTTGAAAACAAGCAGTTGAATACATTGAAAACAAGAAGAAGCATTGAATACATTGAAAACAAGCAATTGATTG	TIGGAGTICGAAGAATCTCCATTGAGCGCTGGCCAATGCTGCCAATGCTGCCGCGGGGGGGG
	113	114	115	116	117
	prey4458	prey4458	prey67522	prey527	prey53735
	ഗ	ည	ഗ	ιo	2
	Shigella ipaC	Shigella ipaC	Shigella ipaC	Shigella ipaC	Shigella ipaC

		ľ	CCGTAGAGGACCTGACAACAACCTCAACGAGGCAGCCAGTGCTGCTGGGG	SAAGVVGGMVDSITQAINQ
		_	TCGTGGGTGGCATGGTGGACTCCATCACCCAGGCCATCAACCAGCTAGATG	LDEGPMGEPEGSFVDYQT
			AAGGACCAATGGGTGAACCAGAAGGTTCCTTCGTGGATTACCAAACAACTAT	TMVRTAKAIAVTVQEMVTK
			GGTGCGGACAGCCAAGGCCATTGCAGTGACCGTTCAGGAGATGGTTACCAA	SNTSPEELGPLANQLTSDY
_		_	GTCAAACACCAGCCCAGAGGAGCTGGGCCCTCTTGCTAACCAGCTGACCAG	GRLASEAKPAAVAAENEEI
			TGACTATGGCCGTCTGGCCTCGGAGGCCAAGCCTGCAGCGGTGGCTGCTG	GSHIKHRVQELGHGCAALV
_			AAAATGAAGAGATAGGTTCCCATATCAAACACCGGGTACAGGAGCTGGGCC	TKAGALQCSPSDAYTKKELI
			ATGGCTGTGCCGCTCTGGTCACCAAGGCAGGCGCCCTGCAGTGCAGCCCC	ECARRVSEKVSHVLAALQA
			AGTGATGCCTACACCAAGAAGGAGCTCATAGAGTGTGCCCGGAGAGTCTCT	GNRGTQACITAASAVSGIIA
			GAGAAGGTCTCCCACGTCCTGGCTGCGCTCCAGGCTGGGAATCGTGGCACC	DLDTTIMFATAGTLNREGT
			CAGGCCTGCATCACAGCAGCCAGCGCTGTGTCTGGTATCATTGCTGACCTC	ETFADHREGILKTAKVLVED
			GACACCACCATCATGTTCGCCACTGCTGGCACGCTCAATCGTGAGGGTACT	TKVLVQNAAGSQEKLAQAA
			GAAACTTTCGCTGACCACCGGGGGGGCATCCTGAAGACTGCGAAGGTGCTG	QSSVATITRLADVVKLGAAS
		_	GTGGAGGACACCAAGGTCCTGGTGCAAAACGCAGCTGGGAGCCAGGAGAA	LGAEDPETQVVLINAVKDV
			GTTGGCGCAGGCTGCCCAGTCCTCCGTGGCGACCATCACCCGCCTCGCTGA	AKALGDLISATKAAAGKVG
		-	TGTGGTCAAGCTGGGTGCAGCCAGCCTGGGAGCTGAGGACCCTGAGACCC	DDPAVWQLKNSAKVMVTN
			AGGTGGTACTAATCAACGCAGTGAAAGATGTAGCCAAAGCCCTGGGAGACC	VTSLLKTVKAVEDEATKGT
			TCATCAGTGCAACGAAGGCTGCAGCTGGCAAAGTTGGAGATGACCCTGCTG	RALEATTEHIRGELAVFCSP
		•	TGTGGCAGCTAAAGAACTCTGCCAAGGTGATGGTGACCAATGTGACATCATT	EPPAKTSTPEDFIRMTKGIT
			GCTTAAGACAGTAAAAGCCGTGGAAGATGAGGCCACCAAAGGCACTCGGGC	MATAKAVAAGNSCRQEDVI
			CCTGGAGGCAACCACAGAACATACGGCAGGAGCTGGCGGTTTTCTGTTC	ATANLSRRAIADMLRACKE
			CCCAGAGCCACCTGCCAAGACCTCTACCCCAGAAGACTTCATCCGAATGAC	AAYHPEVAPDVRLRALHYG
			CAAGGGTATCACCATGGCAACCGCCAAGGCCGTTGCTGCTGGCAATTCCTG	RECANGYLELLD
			TCGCCAGGAAGATGTCATTGCCACAGCCAATCTGAGCCGCCGTGCTATTGC	
			AGATATGCTTCGGGCTTGCAAGGAAGCAGCTTACCACCCAGAAGTGGCCCC	
			TGATGTGCGGCTTCGAGCCCTGCACTATGGCCGGGAGTGTGCCAATGGCTA	
			CCTGGAACTGCTGGAC	
Shigella 5	prey53735	118	CAGTGATGTGCTGGACAAGGCCAGCAGCCTCATTGAGGAGGCGAAAAAGGC 319	SDVLDKASSLIEEAKKAAG
ipac			AGCTGGCCATCCAGGGGACCCTGAGAGCCAGCAGCGGCTTGCCCAGGTGG	HPGDPESQQRLAQVAKAV
-			CTAAAGCAGTGACCCAGGCTCTGAACCGCTGTGTCAGCTGCCTACCTGGCC	TQALNRCVSCLPGQRDVD
			AGCGCGATGTGGATAATGCCCTGAGGGCAGTTGGAGATGCCAGCAAGCGAC	NALRAVGDASKRLLSDSLP
			TCCTGAGTGACTCGCTTCCTCCTAGCACTGGGACATTTCAAGAAGCTCAGAG	PSTGTFQEAQSRLNEAAAG
			CCGGTTGAATGAAGCTGCTGCTGGCTGAATCAGGCAGCACAGAACTGGT	LNQAATELVQASRGTPQDL
			GCAGGCCTCTCGGGGAACCCCTCAGGACCTGGCTCGAGCCTCAGGCCGAT	ARASGREGODESTELEAGY
			TTGGACAGGACTTCAGCACCTTCCTGGAAGCTGGTGTGGAGATGGCAGGCC	EMAGGAPSQEDRAQVVSN
	-		AGGCTCCGAGCCAGGAGCAGCCCAAGTTGTGTCCAACTTGAAGGGCA	LKGISMSSSKLLLAAKALST
			TCTCCATGTCTTCAAGCAAACTTCTTCTGGCTGCCAAGGCCCTGTCCACGGA	DPAAPNLKSQLAAAARAVT
			CCCTGCTGCCCCTAACCTCAAGAGTCAGCTGGCTGCAGCTGCCAGGGCAGT	DSINGLITMCTQQAPGQKE
			AACTGACAGCATCAATCAGCTCATCACTATGTGCACCCAGCAGGCACCCGG	CDNALRELETVRELLENPV

0101011100	320	LESICHAYOLA CLIFENDAY MORE TO BE CLICATE HAS A WORK PECTOR OF CLICATE AND
COGGGAAGGGTGTGATAAGGCCCTGGGGGAATTGGAAGGGTCCGGGGAAAGT CCGGAGAACCAGTCCAAGCGAATTGCTTTGGTTGGTTG GACGGTGAATTGCTCAAGCCATAATTGCAATTGCTTGGTTGG	CACAGGGGCTGACCTGCTAGAAGAGCATCTTGGTGAAATCTGGAACCTGCG CCAGGGCTGGAGGAGTCCATCTGCATCAATGACTGCCTACGGAGCAACT GGAAACCGGC	CATGGAGACTACTO ATO CAGAGAGTA TO COLOGICA AGORDACIO CAGATO CAGAAT CAGAAA CAGATA CAGAGAGAGAGAGAT CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
	119	120
	prey67546	prey4671
	2	ശ
	Shigella ipaC	Shigella ipaC

IDOTSTAT. DILIDE

			CANCOCTORACATACOCOCACACACACACACACACACACACACACACAC	SECTION INCKPTS
			CAACITIECCAGOLAGUI LUCI UCANGEGUALALONI INAANI INGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	ADLLEHLGEIRNLAGRLEE SICINDRLREQLEHR
<u>ب</u>	prey67550	124		MITTELEFHWATPDRUNK AMKRAHDWVEEDOTYVSY DVANKVSEETKKEEKEEKS DOPOEDEKEEKTKEEKEEKS WSSISSLAEVTAROISOLI WKAELILIGOGEEKFAODO AKVIIKITTAMONEVASLSK KFINSLITYGSNKKAEVLN PMISSYLLEGG
<u></u>	prey/8889	22	(5 ()	FONDYORLEHEADYON EAGHEHHOALORIEN VLDANTOKRIKENNERE KKELOKILDAKHNISBEAK MRDKIKKAELTEINREHI ESVINSIRELEADKORHDB LVAGOOOVLOOLEEFEK LAGLAGEOGEGRAFIPOEI BRSILGEREGORGPHO ACASIGHAPGSSGHLSOA BOESOGENTOL
م	prey11375	123	COCTOGGCTGGGGGGGGCTCGGGATTCCCCGAGGAACCCCAAG GCTTGCTGCAGATGGCCATCACCGCGGGCTCTGAAGAGCCAACCTCCAAG GCTTGCTGCAGATGGCCATCACCGCGGGCTCTGAAGAGCCCAAGA GCTGCTTCCCAGAGCCAGCGGGGGTCTGATGGCTGCAGGAGGGCCATGTCC GCGAGTGCTTCCAAGCCCACTGCTGGCGCGCTGGCTTGCT GCGAGTGCTTCCAAGCCCATGCTGCCCCCATGTTGTGGGGAAGGCGCAGCT GCGAGTGCTTCACAAGCCCAAGGGGGGCTGGAACTTGTGGGGAAGGCAGC GCGAGTGCATTGCAAGCCCAAGGGGGGCTTGCTGCAGCAGCTG TGTGAAAAATGGAAATGGAAAGGGGGGCTTGCTGCAGCTTGTTGGCATGCAC GGGCGGAAAATGGAACTTACGCAGCAGGGGTTGCTGCAGGATGGC GGGCGGAAAACTTACGACAACTTGCTGCAGGCTGCAGCTGCAGCAGCTGCAGCAGCTGCAGCAGCAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	SSAGGSGNBRPPRID GGL LOMATAGSEEPDPPPP SEERROWN CAEMSAFRG OREVEGMINGSCHYLSOP MIPTAGEACOADOGER GALELLAGLCEMINDNADF COLSGMILLYGRYLEAGA AGLEWRAACLIGTGSONVA AGLEWCACCOLGCONVA

HODEWIDZ DRAKDR

			17HTELLAGHYBISDPKV IEVELAKHYLKNULAHO ATVETNIKAGNELIESKA DDASSLRSHEAMNOCWE SVLOKTERERGOLOSTLOO SQLASKTGGLPFARE SQLASKTGGLPFARE LDTHMELYSQLKAKEETNY
CCGCGACGCOTGCGACACGGTGCGCGTCAAGGCCCTCTTCGCCATCTCCTG TCTGGTCCGACAGGAGGCTGGGCTG	ATGGCAGAGAGGTGCTGGTAACAGGTGGGCTGGCTACATTGGCAGCCAC 225 ACGGTGCTGCTGGAGCTGGCTGGAGCTGGCTACATTGGCAGCCAC 225 ACGGTGCTGCGAGAGCTGGAGAGGGGGCTGCTTGGCTGTGGTGATGGATTGAGGGGGGGG		GGTGANTOCTANGANTOCTGANGANTOCTACAGAGCCANTACTGGANGC 327 CCGAAAGTCATGAAGTGACGCGAAAGCACCATGTCCTAAAAATGATG TTTTGAATCCTAAAGCTGCAAAGCACCATGTCCTAAAAATGATG TTTTGAATCAAGCCAAGTGGAAACAGCACCAACAAGCTGGCAATGAGCT TCTTGAATCAAGCTGCTGGAAGTATAACAGCAGCAGTTGCAACCAGTTGAACAAGCCTTTGAGCAATTGAACAAGAAGAAGAGAGAG
	124	125	126
	prey67473	prey48929	prey3488
	ω.	LO.	D.
	Shigella ipaC	Shigella	Shigella ipaC

TODESENT DIFFER

			GAACTCTATTCCCAGCTGAAAGCCAAGGAAGAACTTATAATCAACTTGA	0.0	QLLDKGRLMLLSRDDSGS
			CAAGGGCAGACTCATGCTTCTAAGCCGTGACGACTCTGGGTCTGGGTCTCGGCTCCAA	5 K	SSKMEERKSKLEEALNLAT
			TAAGATGGAAAAAAAAAAAAGCTGGAAGGGGCCCTCAACTTGGCAACA	ш	EFONSLOEFINWLTLAEOS
			GAATTCCAGAATTCCCTACAAGAATTTATCAACTGGCTCACTCTAGCAGAGCA	5	LNIASPPSLILNTVLSQIEEH
			GAGTITAAACATCGCTTCTCCACCAAGCCTGATTCTAAATACTGTCCTTTCCC	S	KVFANEVNAHRDQIIELDQT
			AGATAGAAGAGCACAAGGTTTTTGCTAATGAAGTAAATGCTCATCGAGACCA	O	GNOLKFLSOKODVVLIKNLL
			GATCATTGAGCTGGATCAAACTGGGAATCAATTAAAGTTCCTTAGCCAAAAG	<u>~</u>	VSVQSRWEKVVQRSIERG
			CAGGATGTTGTTCTGATCAAGAATTTGTTGGTGAGCGTGCAGTCTCGATGGG	œ	RSLDDARKRAKQFHEAWK
			AGAAGGTTGTCCAGCGATCTATTGAAAGAGGGCGATCACTAGATGATGCCAG	₹.	KLIDWLEDAESHLDSELEIS
			GAAGCGGGCAAAACAATTCCATGAAGCTTGGAAAAAACTGATTGACTGGCTA	Z	NDPDKIKLQLSKHKEFQKTL
			GAAGATGCAGAGTCACCTGGACTCAGAACTAGAGATATCCAATGACCCAG	σ :	GGKQPVYDTTIRTGRALKE
	-		ACAAAATTAAACTTCAGCTTTCTAAGCATAAGGAGTTTCAGAAGACTCTTGGT	Y	KTLLPEDTOKLDNFLGEVH
			GECAAGCAGCCTGTGTATGATACCACAATTAGAACTGGCAGAGCACTGAAAG	Ξ_	DKWDTVCGKSVERQHKLE
			AAAAGACTTTGCTTCCCGAAGATACTCAGAAACTTGACAATTTCCTAGGAGAA	ш	EALLFSGQFMDALQALVD
			GTCAGAGACAAATGGGATACTGTTTGTGGCAAGTCTGTGGAGCGGCAGCAC	≤.	WLYKVEPQLAEDQPVHGD
			AAGTTGGAGGAAGCCCTGCTCTTTTCGGGTCAGTTCATGGATGCTTTGCAGG	_	LDLVMNLMDAHKVFQKELG
			CATTGGTTGACTGGTTATACAAGGTGGAGCCACAGCTGGCTG	₹_	KRTGTVQVLKRSGRELIEN
			CCGTGCACGGGGACCTTGACCTCGTCATGAACCTCATGGATGCACACAGG	S	SRDDTTWVKGQLQELSTR
			TTTCCAGAAGGAACTGGGAAAGCGAACAGGAACCGTTCAGGTCCTGAAGC	3	WDTVCKLSVSKQSRLEQAL
			GGTCAGGCCGAGAGCTGATTGAGAATAGTCGAGATGACACCACTTGGGTAA	Ÿ	KOAEVFRDTVHMLLEWLSE
			AAGGACAGCTCCAGGAACTGAGCACTCGCTGGGACACTGTCTGT	¥.	AEQTLRFRGALPDD1EALQ
			CTGTTTCCAAACAAAGCCGGCTTGAGCAGGCCTTAAAACAAGCGGAAGTGTT	Ö	LIDT
			TCGAGACACAGTCCACATGCTGTTGGAGTGGCTTTCTGAAGCAGAGCAAAC	_	
			GCTTCGCTTTCGGGGAGCACTTCCTGATGACACAGAGGCCCTGCAGTCTCT		
		_	CATTGACACCC		
Shigella 5	prey3514	127	GGAAAAAGAAGAGCTGCCACGTGCCGTGGGTACCCAGACATTGAGTGGTGC 328		EKEELPRAVGTOTLSGAGL
ipaC		_	TGGTCTCCTCAAGATGTTCAACAAAGCCACAGATGCCGTCAGCAAAAIGACC	<u> </u>	- KMIFINAL DAVSKIMI IKMIN
_			ATCAAGATGAATGAATCAGACATTTGGTTTGAGGAGAAGCTCCAGGAGGTAG	ц:	ESDIWFEEKLOEVECEEOR
			AGTGTGAGGAGCAGCGCTTACGGAAACTGCATGCTGTTGTAGAAACTCTAGT	<u> </u>	RKLHAVVETLVNHHKELA
			CAACCATAGGAAAGAGCTAGCGCTGAACACAGAGCCCAGTTTGCAAAGAGTCTA	<u> </u>	NIAGFAKSLAMLGSSEUN
			GCCATGCTTGGGAGCTCTGAGGACAACACGGCATTGTCACGGGCACTCTCC	Η.	TALSRALSQLAEVEEKIEQL
			CAGCTGGCTGAGGTGGAAGAAAAATTGAGCAGCTCCACCAGGAACAGGCC	Ξ.	HOEGANNDFFLLAELLSDYI
			AACAATGACTTCTTCCTCCTTGCTGAGCTCCTGAGTGACTACATTCGCCTCCT	Œ	RLLAIVRAAFDORMKTWOR
			GGCCATAGTCCGCGCTGCCTTCGACCAGCGCATGAAGACATGGCAGCGCTG	<u> </u>	WQDAQATLQKKHEAEAHL
		_	GCAGGATGCCCAAGCCACACTGCAGAAGAAGCGGGAGGCCGAGGCTCGGC		LWANKPDKLQQAKDEILEW
			TGCTGTGGGCCAACAAGCCTGATAAGCTGCAGCAGGCCAAGGACGAGATCC	ш	ESRVTQYERDFERISTWR
			TCGAGTGGGAGTCTCGGGTGACTCAATATGAAAGGGACTTCGAGAGGATTT	<u>×</u>	KEVIRFEKEKSKUFKNHVIK
			CAACAGTGGTCCGAAAAGAAGTGATACGGTTTGAGAAAGAGAAATCCAAGGA	>	YLETLLYSOGOLAKYWEAF

IDD+3487.DIIIDE

		_	CTTCAAGAACCACGTGATCAAGTACCTTGAGACACTCCTTTACTCACAGCAGCCCCCATCCCAAGTACTGGGAAGCCTTCCTT		LPEAKAIS*
Shigella 5 paC	prey5814	128	TIAA TIGATGCCCAGCAGCTIGAAGATGAGGAACCTGCATTTCCAGATACTGAC TIGATGCCCCAGCAGCTIGAAGATGAGGAGCCTCGATGGGTTGGTTTCCAGTTTTTTTT		DAPPOLEDEEPAFPHTDLA KLDDAMINEPRWAVPALPKG ELEVLLEANDLSKKGLDW SEACOTFFEDGLTSFTKIL TDEANSQWKETHFOLVEL CVAKLSODWFETHFOLVEL CVAKLSODWFETHFOLVEL CVAKLSODWFETHFOLVEL CVAKLSODWFETHFOLVEL CVAKLSODWFETHFOLVEL CVAKLSODWFETHFOLVEL CVAKLSODWFETHFOLW THENGEN THENGESALVOUIANLE FETGLEANSCANNUS INCHARKERANIC CARCASTINATAEMAEWIO CONNILSIVITAGEN KARKINGSALVOUIANLE KLINHLANDFSFEGLHTODLD NIWAAQAGKHEANKWHD LLAKLAWDFSFEGLHTODLD LAKLAWDFSFEGLHTODLD KULWINGSKALTLODLD KULWINGSKALTLODLD KULKANDFSFEGLHTONLE KARKILLDYSCSODPHTO KULKULLAKLAWDFSFEGLHTONLE LIKHLADDKOGWAHFW KULKULLAKLADDKOGWAHFW KULKULLAKLADDKOGWAHFW KULKULLAKLADDKOGWAHFW KULKULLAKLADDKOGWAHFW KULKULLAKLADDKOGWAHFW KULKULLAKLADDKOGWAHFW KOMUNDFFEELHTWKWW SQUORSPEGLHTWKWW SQUORSPEGLHTWKWW SQUORSPEGLHTWKWW KOMUNDFFEELHTWKWW KULKULKULKULKULKULKULKULKULKULKULKULKULK
Shigella 5 ipaC	prey5814	129	AAACAAATIRGAGAAATII TAGTIGTITTATICGCCA TCAAACTICGGGGAAAGCCCCATGTTGTTTATICGCCA CCATGCCAAAGCTCCCCATGTGTTTATICGCCA TGGTCCTTCAAGCGTCACAAGTGCTAATCCTAGTCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	30	HAKLGESSLSPSLDSLFFG SASONLYLTEVYALLIMP AGAPLADDSSDFOFHEKS GGLPLVISMLTRINNFLPNA DMETRRGAYLNALKIAKLLL

OFFLMCTRCCMGHRPLLFF GSPPTINAGFELLVALAVGC RGFWKQFRLWGEPVNLRE KALGHPAMLSKVLGGSFAD KRFDYDWERECAIKFNDYF EGDNVNPESQLIQQSEQSE QASGGHYYSYIIQRNGGDG ERNRWYKFDDGDVTECKM DICVIRAIOKIIWASGCGSLQ DVKRTGETGIEETILEGHLG VTKFI I AFOTSEKKFHIGCE KGGANLIKELIDDFIFPASNV VRNLKQIVDSLTEMYYIGTA TGSDVDDDMSGDEKQDNE KVDTVKRLLIKKLPPVLAIQL SETAGSTKYRLVGVLVHSG NVSVRLAGOISDEASRYMP CFALIPTALDALSKEKAWQT ITLLFTVLGSTARERAKHSG DYFTLLRHLLNYAYNSNINV YLOYMRNGELPAEQAIPVC SVIQQLYMIPSIRNGILAIEG EFPRELDMEPYTVAGVAKL TAIGYGHVRAVAEACQPGV VESPNEEITKIYEKTNAGN FPDI EDEGVOCEAL EVMTL -IIDLLLHCHSKTVRQVAQE ITTCEALTEWEYLPPVGPR **PPKGFVGLKNAGATCYMN** SNVDPRDDVFGYPQQFED OKICOGCPHRYECEESFTT INVDIRNHONLLDSLEGYV EGVNPMTQINQVTHDQAV VI OSAI OSIPNPSSECMI B PNAFVI FNNEIDWLKBIRD **KPALSKTEDRKEYNIGVLR** HI OVIFGHI AASBLOYYVP QHDALEFFNSLVDSLDEAL KGDLLEGANAYHCEKCNK **GGTGGATAGTTTAGATGAAGCTTTAAAAGCTTTAGGACATCCAGCTATGCTAA** GTAAAGTCTTAGGAGGTTCCTTTGCTGATCAGAAGATCTGCCAAGGCTGCCC ACATAGGTACGAATGTGAAGAATCTTTTACGACCCTAAACGTAGACATTAGAA GAATTTCCTCGAGAGCTGGACATGGAACCTTACACAGTTGCAGGTGTCGCAA TGTTAAAAGAACAGGAGAAACGGGTATTGAAGAGACGATCTTAGAGGGCCAC CTTGGAGTGACAAAGGAGTTACTGGCCTTTCAAACTTCTGAGAAAAAATTTCA GTTTTGAATTACTTGTAGCATTAGCTGTTGGCTGTGTGAGGAATCTCAAACAA CATTGGTGTCCTAAGACACCTTCAGGTCATCTTTGGTCATTTAGCTGCTTCTC GACTGCAATACTATGTGCCCAGAGGATTTTGGAAACAGTTCAGGCTTTGGGG TGAGCCTGTTAATCTGCGTGAACAACACGATGCTTTAGAATTTTTTAATTCATT GAAGGTGCAAATGCATATCATTGTGAAAAATGCAATAAAAAGGTTGATACCGT AGAGCATTCCTAATCCATCATCCGAGTGCATGCTTAGAAATGTGTCAGTTCGT CTTGCTCAGCAGATATCTGATGAGGCTTCAAGATATATGCCTGATATTTGTGT AGTGATGACCTTATGTTTTGCCTTGATTCCAACAGCCTTAGATGCTCTTAGTA AAGAAAAGGCTTGGCAGACATTCATCATTGACTTACTATTGCACTGTCACAGC CTTTTAAGACACCTTCTTAATTACGCTTACAATAGTAATATTAATGTACCCAAT CCAGCTGAACAGGCTATTCCGGTCTGTGGTTCACCACCTACAATTAATGCTG ATAGTAGATTCTTTGACTGAAATGTATTACATTGGCACAGCAATAACTACTTG GTGATTCAGCAACTCTACATGATTCCTTCCATTAGGAACGGTATTCTTGCCAT GGACAATGAGAGCAATGTTGATCCCAGGGATGATGTATTTGGATATCCTCAA CAATTTGAAGATAAACCAGCATTAAGTAAAACTGAAGATAGAAAAGAGTACAA AAAGCGCTTGCTGATTAAAAATTACCTCCTGTTCTTGCTATACAACTAAAGC GATTTGACTATGACTGGGAAAGAGAATGTGCAATCAAGTTCAATGATTATTT CTCTTAAAATAGCCAAGCTTTTGCTAACTGCCATTGGCTATGGTCATGTTCGA CAGATCAACCAAGTTACCCATGATCAAGCAGTGGTGCTACAAAGTGCCCTTC CTAGTATTTAGCCCAAATGAAGAAATCACTAAAAATTTATGAGAAGACCAATGC AAAACTGTTCGTCAGGTGGCACAGGAGCAGTTCTTTTAATGTGCACCAGAT GTTGCATGGGACACCGGCCTCTACTTTTCTTCATTACTCTACTCTTTACTGTT GCTGAAGTTCTTTTCAATAATGAAATTGATTGGCTTAAAAGAATTAGGGATGA TCATATTTCCTGCATCCAATGTTTACCTACAGTATATGAGAAATGGAGAGTT TGAAGCACTTACTGAGTGGGAATATCTGCCACCTGTTGGACCCCGCCCACC CAAAGGATTCGTGGGGCTGAAAATGCCGGTGCTACTTGTTACATGAATTCT TGAAGGCACAGGTAGTGATGTAGATGATGATGTCTGGGGATGAGAAGCA ATCACCAAAATCTTCTTGATTCTTTGGAACAGTATGTCAAAGGAGATTTACTA GCTGTGGCAGAAGCTTGTCAGCCAGGTGTAGAAGGTGTGAATCCCATGACA AATTAGAGCTATACAAAAATTATCTGGGCATCAGGATGTGGGTCGTTACAG AGGCAATGAGCCAGACTTGGAAGACGAACAGGTTTGCTGTGAAGCATTGGA TATTGGTTGTGAAAAAGGAGGTGCTAATCTCATTAAAGAATTAAATTGATGATT

hand far the brane dee Assemble series and continued the series and the series of the

IKCMVALFSNCPVAYQILQG SPPVQSNETSNGYFLERSH ATSVQQIEMEESKEPDDQD PGSQYQQNNHVHGQPYTG PAAHHMNNPQRTGQRAQE **WWNAYIPFYERMDTIDQDD** NPPLPNPFGDPNLSQPIMPI **NPQFSSTVLSELLWQVAYS** WQTHRIHNALKGIPDDRDG APDEHESPPPEDAPLYPHS VYLNPPPGQDHLLPEAEEIT COYFNLFVMYANLGVAEKT LFDTIQRSKNHYQKRAYQC ELERRPYTGNPQYTYNNW SARMTLAKACELCPEEVKK FI IBYISELAITTRPHOIIMPS ASPGPSSQAYDNLSLSDHL SQLIRCCNVSSRMQSSING YPYELRPYLDLLLQILLIEDS NGDI KRKWTWAVEWLGD **AIERSVRKQNVQFMHNRM** MISIQLAARFLFTTGFHTKK VVRGSASDWYDALCILLRH SKNVRFWFAHNVLFNVSN RESEYLLECPSAEVRGAFA KLIVFIAHFSLQDGPCPSPF LRAVLNLLRREVSEHGRHL QLLKLSVPATFMLVSLDEG **PGPPIKYQYAELGKLYSVV** OONVADILFVRTSYVKKIIE DCSNSEETVKLLRFCCWE QYSMEYFQFMKKLLTCNG DDDEEMKNOCFGGEYMG EVFDHMMKRMSYRRQKR NYEGSEEVSPPQTKDQ* GCAAATCTTACTGATTGAGGACTCCTGGCAAACTCACAGAATTCATAATGCAC TGAAAGGAATTCCAGATGACCGAGATGGGCTGTTTGACACAATCCAGCGCTC TATTTAGTAACTGTCCTGTTGCTTACCAAATCCTGCAGGGCAATGGAGATCTT AAGATGCTCCAGATGAACATGAGTCGCCTCCACCTGAAGATGCCCCATTGTA GGAGTATTTCAGTTTATGAAAAACTGCTTACATGTAATGGCGTTTACTTAAA GTGTACCTGCTACTTTTATGCTTGTGTTTTAGATGAAGGTCCAGGTCCTCCA CTCCTCTCCCAATCCTTTTGGTGATCCTAATTTATCACAACCTATAATGCCAA TTCAGCAGAATGTGGCAGACATTTTATTGTGAGAACAAGTTATGTGAAGAAA ATCATTGAAGACTGCAGTAATTCAGAGGAAACCGTCAAATTGCTTCGTTTTTG CAGGITGCATATTCCTATCCCTATGAACTGCGGCCCTATTTGGATCTGCTTTT TAAGAATCACTATCAAAAAAAGAGCATACCAGTGTATAAAAATGTATGGTAGCTC AGACCATATACTGGCAATCCTCAGTACACTTACAACAATTGGTCTCCCCAGT AGGATGACACTTGCAAAAGCTTGTGAACTCTGTCCAGAGGAGGAGGTAAAAAAG AGCTGGAAGGGGATAATGTAAACCCAGAGAGTCAGTTGATACAACAGAGTGA CCCTCCTCCCGGGCAAGATCACCTGTTGCCTGAAGCAGAAGAAATCACTATG AGGGGTGCGTTTGCAAAACTTATAGTCTTTATTGCACATTTTTCCTTGCAAGA GACAACTTAAGCTTGAGTGATCACTTACTAAGAGCAGTACTAAATCTCTTGAG ATCAAATACCAGTATGCTGAATTAGGCAAATTATACTCAGTAGTGTCACAGCT CTGCTGGGAGAATCCTCAGTTCTCATCTACTGTCCTCAGTGAACTTCTCTGG CCACCAGTGTGCAGCAGATAGAAATGGAAGAGAGCAAAGAGCCAGATGACC GCTCGTACACAGTGGTCAAGCGAGTGGGGGGCATTATTATTCTTACATCATC CAAAGGAATGGTGGAGATGGTGAGAGAAATCGCTGGTATAAATTTGATGATG TTTGGTGGAGAGTACATGGGAGAGAGTGTTTGATCACATGATGAAGCGTATG ATCAGTATTCAACTTGCTGCTAGGTTCCTCTTTACTACAGGATTTCACACAAA GAAAGTAGTCCGTGGCTCTGCCAGTGATTGGTATGATGCATTGTGTATTCTC CTTCGTCACAGCAAGAATGTACGTTTTTGGTTTGCTCATAACGTCCTTTTTAA TGTTTCAAATCGCTTCTCCGAATACCTTCTGGAGTGCCCTAGTGCAGAAGTG GTAATGTATGCCAATTTAGGTGTGGCAGAGAAGACACAGCTTCTGAAATTGA GCAAAGCAATGAAACGTCCAATGGTTATTTCTTGGAGAGATCACATAGTGCT GTGATGTAACAGAATGTAAAATGGATGATGACGAAGAAATGAAAAACCAGTG GTGTACGGAAACAGAACGTACAATTCATGCATAACCGAATGCAGTACAGTAT TGGGCCATGTCCTTCACCTTTTGCCTCTCCTGGACCTTCTAGTCAGGCTTAT TCATACAGGCGCCAGAAAAGGTGGTGGAATGCTTATATACCTTTTATGAAC GCTATCACCACCAGACCTCATCAGATTATTATGCCATCAGCCATTGAGAAAAA GCAGTCTGAAAGTGAGACAGCAGGAAGCACAAAATACAGACTTGTGGGTGT AAGGGAAGTTTCAGAGCATGGGCGTCATTTACAGCAGTATTTCAACCTGTT1

			CCCCCATTCACCTGGATCTCAGATACAACAGATAACCATGTBCATGGACAG CCATATACAGGCCCAGCAGCACATCACATGAACAACCCTCAGAGAACTGGC CAACGAGCAAGAAAAATTATGAAGGCAGTGAAGAAGTATCCCCACCTCAAA	
Shigella ipaC	prey67479	130	331	DELMRHOPTLKTDATTAIIK LLEFICNLGARPSKINAA ERASEDEEEEVOAMOS FRYSTOORTEPNOOWOT ERRIPPLANOYILUMKEVE SILSNNTTDDHCOEFNACK SILSNNTTDDHCOEFNACK SILSNNTTDDHCOEFNACK ERRIPPTS FRYGOGELQLOEDSILSSLEP FRYGOEGLQLOESILSSLEP LHR
Shigella 5 ipaC	prey700	131	332	Midels, Addriving Head Midels, Addriving Head Midels, Addrive Head Midel
Shigella 5 tpaC	prey67481	132		KODOKAPUKEAILHATANL PSYNMDRAAVQTNMHDFQ TELRKILVSQKILALN PDAVELFKKANAMLDEDED ERVDEAALRQLTEMGFPEN RATKALQLNHMSVPQAME WLIEHAEDP
Shigella 5 ipaC	prey67488	133	CETTOATRAMAGNITGAGCGAACAGAGGAGGAGAGAGGAGGTGGACAAAGGAGGAGAGGAGAGAGGAGAGGAGAGAGGAGAGAGAG	LFMKSEHHAAEAQLATAEQ QLRGLRTEAERARQAQSR AQEALDKAKEKDKKITELSK

10043487.011100

					T+ 14 4 C C L C L C L C L C L C L C L C L C
				AAGATCACAGAACTCTCCAAAGAAGTCTTCAATCTTAAGGAAGCCTTGAAGG	EVENTKEALKEUPAALA I P
				AGCAGGCUGGCCGCCCCCCCCCCCCGCGGGGCCGGGGCCCCGGGCCCGGGG	AARDHSSVVALYRSHLLYAI
				GTGGTGGCTTGTACAGAAGCCACCTCCTATGCCATTCAGCATACCT	CO ITAGALI KIDOLI SO
Shigella	ŭ	prey51967	1 34	TGACCAACTIGIGTIGATALIIGCIGGAAAAAIIIIGAAAGAIOAAGAAAAAAAAAAAAA	HGIHDGLTVHLVIKTQNRP
ipac				CAAAACAGGCCTCAGGATCATTCAGCTCAGCAAAATACAGCTGGAAGCA	QDHSAQQTNTAGSNVTTS
				ATGTTACTACATCATCAACTCCTAATAGTAACTCTACATCTGGTTCTGCTACTA	STPNSNSTSGSATSNPFGL
				GCAACCCTTTTGGTTTAGGTGGCCTTGGGGGGACTTGCAGGTCTGAGTAGCTT	GGLGGLAGLSSLGLNTTNF
				GGGTTTGAATACTACCAACTTCTCTGAACTACAGAGTCAGATGCAGCGACAA	SELOSOMOROLLSNPEMM
				CTTTTGTCTAACCCTGAAATGATGGTCCAGATCATGGAAAATCCCTTTGTTCA	VOIMENPFVOSMLSNPDLM
				GAGCATGCTCTCAAATCCTGACCTGATGAGACAGTTAATTATGGCCAATCCA	HOLIMANPOMOCLICHNPE
				CAAATGCAGCAGTTGATACAGAGAAATCCAGAAATTAGTCATATGTTGAATAA	ISHMLNNPDIMROILELAH
				TCCAGATATAATGAGACAAACGTTGGAACTTGCCAGGAATCCAGCAATGATG	NFAMMCEMMKNCCHALS
				CAGGAGATGATGAGGAACCAGGACCGAGCTTTGAGCAACCTAGAAAGCATC	NLESIPGGYNALHEMYIDI
				CCAGGGGGATATAATGCTTTAAGGCGCATGTACACAGATATTCAGGAACCAA	GEPMLSAAGEGFGGNFFA
				TGCTGAGTGCTGCACAAGAGCAGTTTGGTGGTAATCCATTTGCTTCCTTGGT	SLVSNISSGEGSCPSHIEN
				GAGCAATACATCCTCTGGTGAAGGTAGTCAACCTTCCCGTACAGAAAATAGA	RDPLPNPWAPQTSQSSSA
				GATCCACTACCCAATCCATGGGCTCCACAGACTTCCCAGAGTTCATCAGCTT	SSG
Shinella		prev67491	135	AAAGAAAGATGTCAAGCAGCCAGAAGAACTCCCTCCCATCACAACCACAACA 336	KKDVKQPEELPPIIIIISI
				ACTTCTACTACACCAGCTACCAACACCACTTGTACAGCCACGGTTCCACCAC	TPATNITCIATVPPQPQYS
ı i				AGCCACAGATACAGCTACCACGACATCATGTCTATTCCCTTGCGGGCTTGGC	YHDINVYSLAGLAPHII LNP
				ACCACACATTACTCTAAATCCAACAATTCCCTTGTTTCAGGCCCATCCACAGT	TIPLFQAHPQLKQCVRQAIE
				TGAAGCAGTGTGTGCGTCAGGCAATTGAACGGGCTGTCCAGGAGCTGGTCC	RAVQELVHPVVDRSIKIAMT
				ATCCTGTGGTGGATCGATCAATTAAGATTGCCATGACTACTTGTGAGCAAATA	TCEQIVRKDFALDSEESRM
	_			GTCAGGAAGGATTTTGCCCTGGATTCGGAGGAATCTCGAATGCGAATAGCA	RIAAHHMMRNLTAGMAMIT
				GCTCATCACATGATGCGTAACTTGACAGCTGGAATGGCTATGATTACATGCA	CREPLLMSISTNLKNSFASA
				GGGAACCTTTGCTCATGAGCATATCTACCAACTTAAAAAACAGTTTTGCCTCA	LRTASPOGREMMDGAAAQ
				GCCCTTCGTACTGCTTCCCCACAAAGAGAAATGATGATGGATCAGGCAGCTG	LAQDNCELACCFIQKTAVE
				CTCAATTAGCTCAGGACAATTGTGAGTTGGCTTGCTGTTTTATTCAGAAGACT	KAGPEMDKRLATEFELRKH
				GCAGTAGAAAAAGCAGGCCCTGAGATGGACAAGAGATTAGCAACTGAATTTG	ARGEGRRYCDPVVLTYQA
				AGCTGAGAAAACATGCTAGGCAAGAAGGACGCAGATACTGTGATCCTGTTGT	ERMPEQIRLKVGGVDPKQL
				TTTAACATATCAAGCTGAACGGATGCCAGAGCAAATCAGGCTGAAAGTTGGT	AVYEEFARNVPGFLPTNDL
				GGTGTGGACCCAAAGCAGTTGGCTGTTTACGAAGAGTTTGCACGCAATGTTC	SQPTGFLAQPMKQAWATD
				CTGGCTTCTTACCTACAAATGACTTAAGTCAGCCCACGGGATTTTAGCCCA	DVAQIYDKCITELEQHLHAI
				GCCCATGAAGCAAGCTTGGGCAACAGATGATGTAGCTCAGATTTATGATAAG	PPTLAMNPQAQALRSLLEV
				TGTATTACAGAACTGGAGCAACATCTACATGCCATCCCACCAACTTTGGCCA	WLSRNSRDAIAALGLLOKA
				TGAACCCTCAAGCTCAGGCTCTTCGAAGTCTCTTGGAGGTTGTAGTTTTATCT	VEGLLDATSGADADLLLHY

TOCHMENT OF THOM

	USIVITISMETICASALLE LIRISLLIESWIETICASALLE MFANNLYYDTSDSDDYHLL KDLEEGOLIKOTYSKFDINSHH HDALLKNYGLLYCFRKDMD KVEIFIRMYQCRSVEGSC GF*	AAVSVLKPFSKGAPSTSSP AKALPQVRDRWKDLTHAISI LESAKARVTNTKTSKPVHA VKKSPKVRKKRSHVTHRTPK VKKSPKVRKKSYLS	HAINOGASKEWILIN NSLWYKGASKEWILIN SLSWYKGEREKKYMIP SLSWYKGAPUKEGERISWKHY AIPITEGRIWYKGURGIA GDSGLDVOWKASHRAG VYPEKOGAENEDGAGEN SWAIINKSIPDLMPKTIMI SWAIINKSIPDLMPKTIMI MINITKAFIHHELA'N, YS ADOSSIMESADGAGRE DMLRMYHAKRALNIGDIS TSTVSTPVPP	QKQLESNKIPELDMTEVVA PFMANIPLLI YODGPRSK POPKDNGDVCQDCIGMVT DIQTAVRTNSTFVQALVEH VKEECDRLGPGMADICKNY ISQYSEIAIQMMMHMQPKEI
	337	338	95 55 55 55 55 55 55 55 55 55 55 55 55 5	340
(E <	AGACTCTATTCGGALACCTCCAACATGGAGGAAACGCAACAAAATCAAT IS AGACTCTATTCGGALACCCTCCAACATGGAGGAAACGCAACAAAATCAAT IS AGACGCGGTCCGCGTGCTGCTGCTGCTGGAGTCGTGAACGCCGGTGCGGTCCGTGAGGCGTGTAACGATCGTTGATCGCCTTGAGGACTGGAGACTCCAAACGCCGCGGATGAACGCATCCAAACGCCGCGGAATGCAACGCATCCAAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACCAACGCAACCTTCAAACTCCTCAAACTCGCAAACTTGCTTCAAAACTCGCAAACTGCAACGCAATGCATGACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAACTGCTCAAACGCAACTTCAAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAATGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACCTGTGCAACGCAACTGCAACGCAACTGCAACGCAACTGCAACGCAACTTCAACGCAACTTCAACGCAACTTCAACGCAACTTCAACGCAACTTCAACGCAACTTCAACGCAACTTCAACGCAACTTCAACAACTTCAACAACTTCAACAACTTCAACAAC			
	136	137	138	139
	prey323	prey67495	prey67506	prey4578
	ro	2	വ	ഗ
	Shigella ipaC	Shigella ipaC	Shigella paC	Shigella ipaC

IOOTEMB7.OIIIOE

					CALVGFCDEVKEMPMQTL VPAKVASKNVIPALELVEPI KKHEVPAKSDVYCEVCEFI VKEVTKLIDNINKTEKEILDA FDKMCSKLPKSLSEECOE
Shigella ipaC	ശ	prey1135	140		AALVASKYHLGAFESL. AALVASKYTHLGAFESL. ETIIAKOIDHYTKGCVENAD ETIIAKOIDHYTKGCVENAD ETIEGEKKROIDORLEGNINK MEORCLÜDHKYKGAGIGAL ETRILDVFEKTILESNÜVPG MAAYSKIKGSSIMONKOF FINNCOCLIFLÜDPGANSOILERPD FINNCOCLIFLÜDPGANSOILERP FINNKORDILLAMAYGIGFDLY TEALSVEGSTNITGTVPGSE EALVEGDINLAMAYGIGFDLY TEALSVEGSTNITGTVPGSE
Shigella ipaC	വ	prey67465	141	N	TATE WINDS TO SOURCE AND A SOUR
Shigella ipaC	رم د	prey28880	142	AGGITCAGITGACTTATCCAACAAATGITATCCCACCTTITIGGACT 393 TIGTGAGATGATAGAGTGAGAGATGTTATCCGATGGACTAA TIGTGAATATATATAAAATGGATGAAGTTGAGGAGAAACATGGACTAA GAAGAATGTGAGAGTGAAGATGAGGCAGAAACATGTTATA GAAGAATGTGAGAGGCAGAAAATTGAACAACTTCAAATCATGAAAATG GAAGAATGTGAGAGAAAATTGAAGAATGTTGAAAATGTGAAAATG GATTGATGAAAATGAGCTTGAGATCATTGATCAGTTCTTCTCTTCAGAT TIGGATTGAAGACCTAGAGCTTGTTCCAGAGGGAATTCAAGGGGAAACAT TTGGTTTCAATTGCTGCAATGTACCAACAACAAGGGTTCAATTCAAGTCAGTTACAATTTTCAATT	VKDAOVVOVVLDGLSNILK MAEDEAETIGNLEEGGGLE KROLONHENDIYKLAYEII KOLONHENDIYKLAYEII KOGONHENDIYKLAYEII GGGTFGFNSSANVPTEGF GGGTFGFNSSANVPTEGF AVENTONI VARANEETI GG
Shigella	2	prey3599	143	GGCAGTTATTGAGATGTGTCAGTTACTGGTCAIGGGAAAIGAGGAGAGAUUJ344	AVIEWOODEL VINGINEE I EGG

HODEWENT DEFEND

WIKEQAHKFVERYFSSENM LHVFFSSPLPGEEPIGRVEP VGNAPLLALVHKMNNCLSQ QINEDTGTARAIQRKPNPLA VSSGTATAATHAAADLGSP SLQHSRDDSLDLSPQGRLS DVLKRKRLPKRGPRRPKYS OSPKSSFLASLNPKTWGRL STOSNSNNIEPARTAGGSG DGSNPALNVLQRLCAATEQ LNLQVDGGAECLVEIRSIVS ESDVSSFEIGHSGFVKQLLL YLTSKSEKDAVSREIRLKRF TMLKKGNAQNTDGAIWQW YEVYSSSAGPAVRHKCLRA VSSHIASMLSSQDLKIVVGA LOMAEILMOKLPDIFSVYFR REGVMHQVKHLAESESLLT HQDKKSVESTCLCFARLVD NVGOLLVVTPPILSSGMFIM VVRMFSLMCSNCPTLAVQL **ILRIIYFADAELLKDVLKNHA** SPPKACTNGSGSMGSTTS **FPVKSVVPALITLLQMEHNF** DIMNHACRALTYMMEALPR SKAILOAGGLADCLLYLEFF MKQNIAETLHFLLCGASNG TSI ICEI MPCI PKEGIFAVD MKEDPELAKSFIKTLFGVL SSAVVVDAIPVFLEKLQVIQ CIDVAEQALTALEMLSRRH SINAGRNALAIAANCCOSIT PDEFHFVADSLPLLTQRLT NFOHEENLLOQVASKDLLT SCOEQIDLVPRSPQELYEL RDDRGLWHPYNRIDSRIIE NSNTSGYSESKKDDARAQ PPRDDDKVDNQAKSPTTT ARAASKDTISNNREKIKG ACATGGGGAAGGTTAAGTACACAGTCCAACAGCAACAACATTGAGCCAGCAC TGGTGGAGCTGAGTGCCTTGTAGAAATCCGTAGCATAGTCTCAGAGTCAGAT CATCAAGTAAAACACTTAGCAGAATCAGAGTCTTTGTTGACAAGTCCACCAAA CCACCACTACTCAGTCACCTAAAATCTTTCCTGGCAAGCTTGAATCCAAAA ATGTCCTTCAGAGACTTTGTGCTGCAACCGAACAACTCAACCTCCAGGTGGA GGGATGTTTATAATGGTGGTTCGCATGTTTTCTCTGATGTGTTCCAACTGTCC ACGAAGCCCTCAAGAGTTGTATGAACTGACATCTCTGATTTGTGAACTTATGC CATGTTTACCAAAAGAAGGCATTTTTGCAGTTGATACCATGTTGAAGAAGGGA AATGCACAGAACACAGATGGTGCGATATGGCAGTGGCGTGATGATCGGGGC GCTTATGAAAGAGGATCCGGAACTGGCTAAGTCTTTTATTAAGACATTATTTG GTGCCTTAGAGCAATTCTTAGGATAATTTATTTTGCGGATGCTGAACTTCTGA AGGATGTTCTGAAAAATCATGCTGTTTCAAGTCACATTGCTTCCATGCTGTCA AGCCAAGACCTGAAGATAGTAGTGGGAGCACTTCAGATGGCAGAAATTTTAA TGCAGAAGTTACCTGATATTTTAGTGTTTACTTCAGAAGAGAAGGTGTAATG TGGGACAGCCACAGCTGCCACTCATGCTGCAGCTGACTTGGGATCACCCAG CTTGCAGCACAGCAGGGATGATTCTTTAGATCTCAGCCCTCAAGGTCGATTA GGACTGCGGGAGGTAGTGGCCTTGCCAGGGCTGCCTCAAAGGATACCATCT CCAATAATAGAGAAAAAATTAAAGGTTGGATTAAGGAGCAGGCACATAAATTT GTAGAACGTTATTTCAGTTCTGAGAATATGGATGGAAGCAACCCTGCATTGA GGAGGGTTTCCTGTCAAGAGTGTTGTTCCAGCTTTGATTACGTTACTTCAGAT GAATTTCATTTTGTGGCAGATTCACTCCCATTGCTAACCCAAAGGCTAACACA TCCTGTGTGGTGCCTCCAATGGAAGTTGTCAGGAACAGATTGATCTTGTTCC CTCTGGCATCCATATAACAGGATTGACAGCCGGATCATTGAGCAAATCAATG ATAGT AACACTAGT GGAT ATT CAGAGT CAAAGAAGGAT GAT GCT CGAGCACA GTGTTCTTTATGAAGTGTATAGTTCCTCAGCAGGACCTGCGGTCAGACATAA AGTGATGTTCTAAAGAGAAAACGACTGCCAAAAACGAGGGCCAAGAAGGCCA AAGTACTCACCTCCAAGAGATGATGACAAAGTAGACAATCAAGCTAAAAAGCC TTAGAAAAGCTGCAAGTTATTCAGTGTATTGATGTGGCAGAGCAGGCCTTGA GTGGTTTGGCAGACTGCTTGCTGTACCTAGAATTCTTCAGCATAAATGCCCA ICAGGATAAAAAGTCAGTAGAAAGCACTTGCCTTTGTTTTGCACGCCTAGTG GACAACTTCCAGCATGAGGAGAATTTACTCCAGCAGGTTGCTTCCAAAGATC IGCTTACAAATGTTCAACAGCTGTTGGTAGTGACTCCACCCATTTTAAGTTCT AACTITAGCTGTTCAACTTATGAAACAAAACATTGCAGAAACGCTTCACTTTC AGGACACGGGAACAGCACGTGCCATTCAGAGAAAACCTAACCCGTTAGCCA TGGAAGCACTTCCTCGATCTTCTGCTGTTGTAGTAGATGCTATTCCTGTCTT AAGAAATGCATTAGCAATTGCAGCTAATTGCTGCCAGAGTATCACGCCAGAT CTGCCTTGGAGATGTTGTCACGGAGACATAGTAAAGCCATTCTACAGGCGG Dad

	ATTTOTTOTONOOMACTOTTTA	MEDEPVKYHDEPSGNGTG
	GTITCALCALITERARICCARCALGEGALITETERAGGAGAGAGATTAAAG	GSFSLNRGSQALKFFNTHQ
	CGATTTCTTCATGTATTTTTTCTTCTCCACTTCCTGGAGAGAGCCCATTGG	LKCQLQRHPDCANVKQWK
	AAGAGTGGAACCAGTGGGTAATGCACCTTTGTTGGCATTAGTTCACAAGATG	GGPVKIDPLALVQAIERYLV
	AACAACTGCCTCAGCCAGATGGAACAATTTCCAGTCAAAGTACATGTCC	VRGYGRVREDDEDSDDDG
	CTAGTEGAAATGGGACAGGAGGCAGCTTTTCTCTCAACAGAGGATCACAGG	SDEEIDESLAAQFLNSGNV
	CTTTAAAAATTTTTCAACACACACATTAAAATGCCAGTTACAAAGGCATCCA	RHRLOFYIGEHLLPYNMTV
	GACTGTGCAAATGTGAAGCAGTGGAAGGGTGGACCTGTCAAGATTGACCCT	YQAVRQFSIQAEDERESTD
	CTGGCTTTGGTACAAGCCATCGAGATACCTTGTAGTTAGAGGGTATGGAA	DESNPLGRAGIWTKTHTIW
	GAGTAAGAGAAGATGATGAAGACAGCGATGACGATGGATCAGATGAGAAA	YKPVREDEESNKDCVGGK
	TAGATGAGTCTCTGGCTGCTCAGTTCCTAAATTCAGGAAATGTAAGACACAG	RGRAQTAPTKTSPRNAKK
	GCTGCAGTTTTATATATGGAGAACATTTGCTGCCGTATAACATGACTGTATAC	HDELWHDGVCPSVSNPLE
	AGGCAGTACGGCAGTTTAGTATACAGGCTGAAGATGAAAGAGAATCCACAGA	VYLIPTPPENITFEDPSLDVI
	TGATGAGAGCAATCCTCTAGGCAGAGCTGGTATTTGGACAAAGACTCATACA	LLLRVLHAISRYWYYLYDNA
	ATATGGTATAAACCTGTGAGAGAGGATGAAGAAAGTAATAAAAGATTGTGTTG	MCKEIIPTSEFINSKLTAKAN
	GTGGTAAAAGAGGAAGAGCCCAAACAGCTCCAAGGAAACTTCCCCTAGAAA	ROLODPLVIMTGNIPTWLI
	TGCAAAAAAGCATGATGAGTTATGGCACGATGGAGTGTGCCCATCAGTATCA	ELGKTCPFFFPFDTRQMLF
_	AATCCTTTAGAAGTTTACCTCATTCCCACACCACCTGAAAATATAACATTTGAA	YVTAFDRDRAMORLLDTNP
_	GACCGTCATTAGATGTGATCCTTCTTTTAAGAGTTTTACATGCTATCAGTCG	EINGSDSGDSRVAPRLDRK
	ATACTGGTATTACTTGTATGATAATGCAATGTGCAAGGAAATTATTCCAACTA	KRTVNREELLKQAESVMQ
	GTGAATTTATTAACAGTAAGTTAACAGCAAAAGCAAATAGGCAACTTCAAGAT	DLGSSRAMLEIQYENEVGT
	CCTTTAGTAATCATGACAGGAAACATCCCAACATGGCTTACTGAGCTAGGAA	GLGPTLEFYALVSQELQRA
	AAACCTGCCATTTTCTTTCCTTTTGATACCCGGCAAATGCTTTTTATGTAA	DLGLWRGEEVTLSNPKGS
	CTGCATTTGATCGGGACCGAGCAATGCAAAGATTACTTGATACCAACCCAGA	QEGTKYIQNLQGLFALPFG
	AATCAACCAGTCTGATTCTCAAGATAGCAGAGTTGCACCTAGATTGGATAGA	RTAKPAHIAKVKMKFRFLG
	AAAAAAGGTACTGTGAACCGAGAGAGCTGCTGAAACAGGCGGAGTCTGTG	KLMAKAIMDFRLVDLPLGLP
	ATGCAGGACCTCGGCAGCTCACGGGCCATGTTAGAAATCCAGTATGAAAATG	FYKWMLRQETSLTSHDLFD
	AGGTTGGTACAGGTCTTGGGCCTACACTGGAGTTTTATGCGCTTGTATCTCA	IDPVVARSVYHLEDIVROKK
	GGAACTACAGAGAGCTGACTTGGGTCTTTGGAGGGGGGAGGAGGAAGTAACTCTT	RLEODKSOTKESLOYALET
	AGCAATCCAAAAGGGAGCCAAGAAGGGACCAAGTATATTCAAAACCTCCAGG	LTMNGCSVEDLGLDFTLPG
	GCCTGTTTGCGCTTCCCTTTGGTAGGACAGCAAAGCCAGCTCATATCGCAAA	FPNIELKKGGKDIPVI IHNLE
	GGTTAAGATGAAGTTTCGCTTCTTAGGAAAATTAATGGCCAAGGCTATCATG	EYLRLVIFWALNEGVSRQF
	GATTTCAGATTGGTGGACCTTCCCCTTGGCTTACCCTTTTATAAATGGATGCT	DSFRDGFESVFPLSHLQYF
	AGGGGAAGAAACTTCACTGACATCACACGATTTGTTTGACATCGACCCAGTT	YPEELDQLLCGSKADTWD
	GTAGCCAGATCAGTTTATCACCTAGAAGACATTGTCAGACAGA	AKTLMECCRPDHGYTHDS
	TTGAACAAGATAAATCCCAGACCAAAGAGAGTCTACAGTATGCATTAGAAAC	HAVKFLFEILSSFUNEGORL
	CTTGACTATGAATGGCTGCTCAGTTGAAGATCTAGGACTGGATTTCACTCTG	FLOFVI GSPALPVGGFRSL
	CCAGGGTTTCCCAATATCGAACTGAAGAAAGGAGGGAAGGATGTACCAGTCA	I DEVATOVNYI KI POVSSIE
	CTATCCACAATTTAGAGGAGTATCTAAGACTGGTTATATTCTGGGCACTAAAT	

FOOTERST OFFICE

ADDITATE OLITIC

	MaiGLSAGONMANT-POW MAIGLSAGONMANT-POW GTGOPYGPTFTTGDNIGCC VALINNTCRYAGIAGTA FTDL-PPNLYPTYGLOTPGE FTDL-PPNLYPTYGLOTPGE FEWGTYKROAGIPFFEIGDPY HEWFTKROAGIPFFEIGDPY HGYCATAE	MGGLESRHATKRSTVEVI ESIDKEIOALEFFEKNORL OKLWVGRLILYSSVLYLTG LIYYLWYLDETARLAMT PFFAPLIWSIRTVIIFFESK RTERNNEALDDLKSORKKI LEEVMEKETYKT	MGDNG INVEKASNIKKI TWLGKRDEVDHIDLUDPV LTCAFINGEDLDULGLTF RKDLFANNOSFEPAFEDK RKDTRLGGEHAVP FTEEPPRLPSSYLOPGFE DTGKAGGVDYEVKAFCAE DTGKAGGVDYEVKAFCAE DTGKAGGVDYEVKAFCAE MSDKPLLEASLDKEIYH GEPISWNHYTNIKTWY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KKISWPGYADICLENTAGY KUSWPG
	346	347	848
AGGITGCAGTGAGCCGAGATCGAGCCACTACTGTCCAGCCCGGCGGCAGT			
	145	146	147
	prey700	prey67718	ps/5230
	9	φ	Ø
	Shigella ipaH9.8	Shigella ipaH9.8	Shige lia

		_		STATE OF TAXABLE DAY
		_	CGTGGCCGTGGAACTGCCCTTCACCCTAATGCACCCCAAGCCGAAAGAGGA	DIVEEDFARGELKGWIKDUN
			ACCCCGGCATCGGGAAGTTCCAGAGAACGAGACGCCAGTAGATACCAATCT CATAGAACTTGACACAAATGATGACGACATTGTATTTGAGGACTTTGCTCGCC	EEEEDGI GSPOLNNH
			AGAGACTGAAAGGCATGAAGGATGACAAGGAGGAGGAGGAGGAGGATGGTACCG GCTCTCCACAGCTCAACAACAGATAG	
ď	prev67731	148	ATGTCAATAGCAGGAGTTGCTGCTCAGGAGATCAGAGTCCCATTAAAAACTG 349	MSIAGVAAQEIRVPLKTGFL
			GATTTCTACATAATGGCCGAGCCATGGGGAATATGAGGAAGACCTACTGGAG	HNGRAMGNMRKTYWSSR
		_	CAGTCGCAGTGAGTTTAAAAACAACTTTTTAAATATTGACCCGATAACCATGG	SEFKNNFLNIDPITMAYSLN
			CCTACAGTCTGAACTCTTCTGCTCAGGAGGGCCTAATACCACTTGGGCATGC	SSAGERLIPLGHASKSAPM
		Ė	TTCCAAATCTGCTCCGATGAATGGCCACTGCTTTGCAGAAAATGGTCCATCT	NGHCFAENGPSOKSSLPPL
		_	CAAAAGTCCAGCTTGCCCCCTCTTCTTATTCCCCCAAGTGAAAACTTGGGAC	LIPPSENLGPHEEDQVVCG
			CACATGAAGAGGATCAAGTTGTATGTGGTTTTAAGAAACTCACAGTGAATGG	FKKLTVNGVCASTPPLTPIK
_			GGTTTGTGCTTCCACCCCTCCACTGACACCCATAAAAAACTCCCCTTCCCTTT	NSPSLFPCAPLCERGSRPL
			TCCCCTGTGCCCCTCTTTGTGAACGGGGTTCTAGGCCTCTTCCACCGTTGCC	PPLPISEALSLDDTDCEVEF
			AATCTCTGAAGCCCTCTCTCTGGATGACACAGACTGTGAGGTGGAATTCCTA	LTSSDTDFLLEDSTLSDFKY
			ACTAGETEGATACAGACTTCCTTTTAGAAGACTCTACACTTTCTGATTTCAA	DVPGRRSFRGCGQINYAYF
			ATATIGATICT CONTROL AND A SECTION OF THE SECTION OF	DTPAVSAADLSYVSDQNG
			ACATATTTTGATACCCCAGCTGTTTCTGCAGCAGATCTCAGCTATGTGTCTGA	GVPDPNPPPPQTHRRLRR
			CCAAAATGGAGGTGTCCCAGATCCAAATCCTCCACCTCAGACCCACCGA	SHSGPAGSFNKPAIRISNC
			AGATTAAGAAGGTCTCATTCGGGACCAGCTGGCTCCTTTAACAAGCCAGCC	CIHRASPNSDEDKPEVPPR
			TAAGGATATCCAACTGTTGTATACACAGAGCTTCTCCTAACTCCGATGAAGAC	VPIPPRPVKPDYRRWSAEV
			AAACCTGAGGTTCCCCCAGAGTTCCCATACCTCCTAGACCAGTAAAGCCAG	TSSTYSDEDRPPKVPPREP
			ATTATAGAAGATGGTCAGCAGAAGTTACTTCGAGCACCTATAGTGATGAAGA	LSPSNSRTPSPKSLPSYLN
			CAGGCCTCCCAAAGTACCGCCAAGAGCCTTTGTCACCGAGTAACTCGCG	GVMPPTQSFAPDPKYVSS
		_	CACACCGAGTCCCAAAAGCCTTCCGTCTTACCTCAATGGGGTCATGCCCCC	KALQRQNSEGSASKVPCIL
_			GACACAGAGCTTTGCCCCTGATCCCAAGTATGTCAGCAGCAAAAGCACTGCAA	PIIENGKKVSSTHYYLLPER
_			AGACAGAACAGCGAAGGATCTGCCAGTAAGGTTCCTTGCATTCTGCCATTA	PPYLDKYEKFFHEAEE ING
			TTGAAAATGGGAAGAAGGTTAGTTCAACACATTATTACCTACTACCTGAACGA	GACIQFLPADCGISSALERP
			CCACCATACCTGGACAAATATGAAAATTTTTAGGGAAGCAGAAGAAAAAAAA	DSKI KMDLGGHVKHKHLS
			TGGAGGCGCCCAAATCCAGCCATTACCTGCTGACTGCGGTATATCTTCAGCC	YWSP*
			ACAGAAAAGCCAGACTCAAAAAAAAAAGGATCTGGGTGGCCACGTGAAG	
			CGTAAACATTTATCCTATGTGGITTCICCIIAG	APO IN SEAL OF BIANDEA
9	prey7155	149	GCTCCCGGACGTCCCTGCTCCTGGCT111GCCC1GC1C1GCC1GCC1GC	GAVOTVPLSRLFDHAMLQA
			CARGAGGG GG GCG CCARACCG CCACAGGG CCACGGG CCACGG CCA	HRAHQLAIDTYQEFEETYIP
			GGAGTTTGAAGAAACCTATATCCCAAAGGACCAGAAGTATTCATTC	KDQKYSFLHDSQTSFCFSD
			GACTOCCAGACCTCCTTCTGCTTCTCAGACTCTATTCCGACACCCTCCAACA	SIPTPSNMEETQQKSNLEL
			TGGAGGAAACGCAACAGAAATCCAATCTAGAGCTGCTCGGCATCTCCCTGCT	LAISTELIESWEE VIII EI IS

ECTTED Zenshoot

					1 11 11 11 11 11 11 11 11 11 11 11 11 1
				GCTCATCGAGTCGTGGCTGGAGCCCGTGCGGTTCCTCAGGAGTATGLICGC	MPANINLY TO I SUSDO THEE KDLEEGIQTLMGVRVAPGV
					ANPGTPLA*
		100,	5	CCTCCACCGGTTGAACTGCG 351	EYDAERPPSKPPPVELRAA
Shigella	9	prey168/	2		ALRAEITDAEGLGLKLEDRE
ipans.o					TVIKELKKSLKIKGEELSEA
					NVRLSLLEKKLDSAAKDAD
					ERIEKVOTRLEETOALLRKK
					EKEFEETMDALQADIDQLE
					AEKAELKORLNSOSKRTIE
					GLRGPPPSGIATLVSGIAGE
			_		EGGRGAIPGGAPGSVPGP
	_		_		GLVKDSPLLLQQISAMHLHI
					SQLQHENSILKGAQMKASL
					ASL
Shinella	g	prev67734	151	352	MSQRDTLVHLFAGGCGGT
Blagaria Barri	,				VGAILTCPLEVVKTRLQSSS
2					VTLYISEVOLNTMAGASVN
					RVVSPGPLHCLKVILEKEG
					PRSLFRGLGPNLVGVAPSH
					AIYFAAYSNCKEKLNDVFD
					PDSTQVHMISAAMAGFTAI
					TATNPIWLIKTRLQLDARNR
					GERRMGAFECVRKVYQTD
					GLKGFYRGMSASYAGISET
					VIHFVIYESIKOKLLEYKTAS
					TMENGEESVKEASUFVGM
					MLAAATSKTCATTIAYPHVV
					RTRLREEGTKYRSFFOILS
				ATATCCACATGTTGTAAGAACAAGACTACGTGAAGAGGGAACAAAATACAGA	LLVQEEGYGSLYRGLTTHL
				TCTTTTTTCAGACTCTATCTTTGCTTGTTCAAGAAGAAGGTTATGGGTCTCTT	VRQIPNTAIMMAI YELVVYL
				TATCGTGGTCTGACACTCATCTAGTGAGACAGATTCCAAACACAGCCATIAI	LNG.
					L
Shigella	9	prey2694	152	323	MAHAMENSW IISKEYHIDE
ipaH9.8					WMFIAKHI PDI JESGOJ BE
				TATAATGACTGGATGIICAIIGCIAAACAICIGCCIGAICICAIAGAGATCATCA	BVFKI NMLSIDHLTDHKSQ

HODGENERY LONGED

RIARIU GGITMAYWIGKG HIGDHRWLPRINAVPYCOL SKKIELPPILVADOVLANW KKKOPNKHTTFRMINDLFS FRODCSKGFFLVSLLVER AASAKVIPTVFKAMOMOE NPOTLIKAALLEJASCLEKALO VFHQIPDHN	XXTICXXVEIGHAUKGMVH VSLNCITWXHXLYXVXVHF VBSDLSALXXXXXXXCX SVYXTXX*YLXVIXXXXXX GXGXRXFXLCTXXGG	PUDDESFEGNKÄYRTWYA KLDEEARUNATVORTHLA AAVPENAYYKESOGNSTR IDYGTGHEAFAAFLCOLG KIGNLANDDIAVIKKYNR YLENNRKCIACHYRMEPAG SGGVWGLDDFGFLPFIWG SSQLIDH	DKLSOAKAYCNLGLAFKAL LNFSKAECCXPTVPSPV SE*FPG*ISSPRKPGHYIH! KRYKWCNKIL*AATGLSSP GKGOKIRSOCICSP	SINDADERICATORAGE SINDADERICATORAGE SILADODLKIFSHSPVGRRM PLWCWSHSNGSALVRMAL HPORSDVYKSDDDKTLPVII GEVOAAFVKLKQLCVNEPF
	354	2	326	357
	NGGACAGGGGGATG STCTATACCNAGITNG CINTINCCNTCTTCC CIGANTGTACTTANTG CGCNTTTTNTTCTGT			
	153	45	35	156
	prey67740	prey67703	prey67741	prey67742
	9	9	9	· ω
	Shigella ipaH9.8	Shigella ipaH9.8	Shigella ipaH9.8	Shigella ipaH9.8

TIDATES CILLE

					VI IMOTIVE OF INVITATION
				CATTTGTAAAACTGAAGCAGCTATGCGTTAATGAGCCTTTAGAATATGAAGGG	VBAFI KHSAFI VYMLESKH
				GAGAAAIGGIIAICIICACIGGAAAAIACICAAIGGAAAGGAAAGGAAACATCTC	LSVVLQEEEGRDLSCCVAS
				CALLICOLLANGUAL I CANGOAGAACH I GLALIACA I GCACTGACTGATGACTTGAGCTGATGAGCTT	LVQVMLDPYFRTITGFQSLI
				CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	QKEWVMAGYQFLDBCNHL
				ACTOT BY I CARGINAL INC. ACTO ACTO ACTO ACTO ACTO ACTO ACTO ACTO	KRSEKESPLFLLFLDATWQ
				AGIOLOGAL ACADA ACADA ACADA ACADA CONTROLLA CO	LLEQYPAAFEFSETYLAVLY
				GOARGOALOLARAGACTETTAGAACAATATCCTGCAGCTTTTGAGTTCTCCG	DSTRISLFGTFLFNSPHQRV
				AAACCTACCTGCAGTGTTGTATGACAGCACCCGGATCTCACTGTTTGGCAC	KQSTVSRIKSCTKQDYFPS
				CTTCCTGTTCAGCTCCCCTCACCAGCGAGCAAGCAAAGCACGGTCAGTAG	₽V*
				CATABABAGTTGTACABABAGAGATTATTTCCTTCACGAGTTTGA	
		00000	167	CENAGRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	EEEETELPTVPPVPTEPSP
Shigella	·o_	preyo/338	6	CAPTOCOATECCAGACCCTTGCAGTAGTGGAACTGGATGCCATGATGCTGGG	MPDPCSSELDAMMLGPRG
грану.8				CAGI COOKI GOAGAGAGATA TAGATTA AGGGGGACTATGT GTGTGGACTGTATC	KTYAFKGDYVWTVSDSGP
				A A TITCA GAACC GAGCCCTTG TTCCGAGTGTCTGCCCTTTGGGAGGGGGCT	GPLFRVSALWEGLPGNLDA
				COCCEDA A A COT GAT GOT GOT GT CT A CT C G C C C G A C C A T G G A T T C A C	AVYSPRTQWIHFFKGDKV
			_	TTCTTT A A COGA A CALA A GOTT GEORGE TA CATT TO CA GA TGT CT CT G	WRYINFKMSPGFPKKLNRV
			_	OCT TO COMPANY AND TANGED TARABLE TARABBE TARABLE TARABLE TARABLE TARABLE TARABLE TARABLE TARABLE TARABBE TARA	EPNLDAALYWPLNQKVFLF
				GCT CCCCAACAACAACAACAACAACAACAACAACAACAACAA	KGSGYWQWDELARTDFSS
				TIGGCCICICAACCAAAGGII COIIOIII OOGGGGGGGGGGGGGGGGGGGGGGGG	VPKPIKGI FTGVPNOP
				TGGGACGAGCI AGCCCGAACI GACI I CAGCAGCI ACCCCAAACCAA	3
				GGTTTGTTTACGGGAGTGCCAAACCAGCCC	TO ICIOA O A CONTROLL
Shinolla	4	prev67337	158	GGCTCCCTTGACCTTCCAAGAGGTGCAGGCTGGTGCGGCTGACATCCGCC 359	APLI FOEVQAGAADIRLSF
in a Heni				CTCCTTCCATGGCCGCCAAAGCTCGTACTGTTCCAATACTTTTGATGGGCCT	HGHQSSYCSNIFDGFGHV
200				GGGAGAGTCCTGGCCCATGCCGACATCCCAGAGCTGGGCAGTGTGCACTTC	LAHADIPELGSVHFDEDEF
				GACGAAGACGAGTTCTGGACTGAGGGGACCTACCGTGGGGTGAACCTGCG	WTEGTYRGVNLRIIAAHEV
				CATCHER CONTROL OF THE CONTROL OF TH	GHALGLGHSRYSQALMAP
				CALL GOLDON AT A CONTROL OF THE CALL OF TH	VYEGYRPHEKLHPDDVAGI
				A I I CUCAGGOCO CONTRA GALOCOCONTRA CONTRA C	OAI YGKKSPVIRDEEEET
				TAAGCI GCACCCAGAI GAI GAI GAGCAGAGAGAI COCO COCO COCO COCO COCO COCO COCO CO	EI PTVPPVPTFPSPMPDPC
				GAGTCCAGTGA AAGGGA GAGGAAAGAAGAAGAGACAGAGAGAGAGAG	SSEL DAMMI GEAPPI DAV
				GCCCCCAGAGACCCAGACCCAAGACCAAGACCCAAGACCAAGACCAAGACCAAGACCCAAGACAACA	GBEWGODADPFAWTNGS
				ACTGGATGCCATGATGCTGGGTGAGGCCCCICCCCICCAGGCTGTTGGAGGCAGG	DWG! OHEOWBAPWED! C
				GCGGTGGGGGCAGCCTGCTGATCCTGAGGCCTGGACAAA I GGGAGGGGG	COCCI CANCIDED TO VE
				TGGGACTTCAGCATGAGCAATGGAGGCCCCGTGGGAAGACCIAIGCIIIC	FGGGLCVDCINI GFLVI
				AAGGGGGACTATGTGTGGACTGTATCAGATTCAGGACCGGGCCCCTTGTTC	SVCPLGGAPHKPGCCCLLA
				CGAGTGTCTGCCCTTTGGGAGGGGCTCCCCGGAAACCTGGATGCTGCTGTC	SNIMDSLL
				TACTOGCCTCGAACACAATGGATTCACTTCTTTAA	
Shigella	9	prey67746	129	ATGGAGAATATTCAATAATGAGGCATGAATATGCATGGAAAAAAGGAAA 360	MEKYSIMKSMINMHRKKGK RTILEMTQILKRHGYCTLGE
ipaH9.8				AAGGACCATTAATCGGTTAGACTTCTCAAGTGCAATTCAAGATATCCG	AFNRLDFSSAIQDIRTFNYV

IDD43487.011102

711740110111	361		363	TACCC TRACCC TRACCC KKWKGNRWKRIPLLTIOK GGGAA GGGAA GGGAA GGGAA GCHEGDGATDGPARLLIO GTALPDKVPRDMRGCF
ANCOTTCAATTATGTGGTCAAACTGTTGCAGCTAATTGCAAAATCCCAGTTAA CITCAATTGATGGCGTGGCAGAAGAAATTATCTCAACATTTGGATAAAATC GTTCAAAGGGTTGTATGAGACAAATTCTTCAACATTAATCAAAGTTCTTCAACATTGAATCTTTTGGATGAAAATTCTTCAATTAATGGAAACTTTTTGGATTGCCAATTAAAACTTTTTGGAATTCTTTAATCAAACTTTTTGGAATTCTTTTTTAATCAAACTTTTTGGAATTCTTTTTTTT	GCTGTCCAAAACCAACAGGACCCTCTTTATATTTGGTGTCACAAAGTATTTG CAGGACCTATCAATGTGAAATTGGAACCCCGTGGAGTGCCAGCGACGAGTG ACCCAGTCAACCTGTCAATGTCATCATCAAACTTCCCCAGCATTTACCC TTCAATTCAA	ÄÄGÄÄÄTTÄÄGTÄTTÄGÄÄÄTTTÄGÄÄÄTTÄÄÄÄÄTTÄÄÄÄÄTTÄÄÄÄÄTTÄÄÄÄÄTTÄÄÄÄÄTTÄÄÄÄ	GEAGGCAGACAAGACTGTCTTAAAAAAAGGAAAAAATGGAAAAACTGGACAAG AATCATGTGGGAGAAGGCAGAACATCCTGTGATGGGTCAATAATGACCA ATTCATGGACQACAGTGATGAGGAAAAAGGGATTGTGAGTGCCAGGAAGGCA AGTTTCGAACAACGTGGCAAGGAAAAGGGAAGCCTGTGAGAACGGGCCTTTG AGCCGGAAACTGAGGAAGGAAGCAGGCTGTGAGAACGGGGCCTTTG AGCCGGAAACTGAGGAAGGAGTTGAGCCTGGGGCTCTTGGGGGGTGCAGTG	GGGTGAGCCACCGTCCCCTTACCTCTGCCACTGCCCTATCCATCC
\$000000F404F4F	001	161	162	163
	prey54430	prey67749	prey67751	prey8739
	ဖ	9	9	9
	Shigella ipaH9.8	Shigella ipaH9.8	Shigella ipaH9.8	Shigella ipaH9.8

IODKIHBY DILIDE

				A CTG A T G G G C T G C T G C T G A A C C T G A C C T G A	DEDLWVHENCALWSIEVT
				CTCAACTGTGCCTTTGGTCCACGGAGGTGTATGAGACCCAGGGCGGAGCA	ETGGGALMNVEVALHHGLL
				CTGATGAATGTGGAGGTTGCCCTGCACCGAGGACTGCTAACCAAGTGCTCC	TKCSLCQRTGATSSCNRM
				CTGTGCCAGGGAACTGGTGCCACCAGCAGCTGCAATCGCATGCGTTGCCCC	RCPNVYHFGCAIRAKCMFF
				AATGICIACCATTITGGTTGTGCCATCCGCGCCAAGTGCATGTTCTTCAAGG	KDKTMLCPMHKIKGPCEQE
				ACAAGACCATGCTGTGTCCAATGCATAAGATCAAGGGGCCCTGTGAGCAAG	LSSFAVFRR
				AGCTGAGCTCTTTTGCTGTCTTCCGGCGGG	MUSICALLISONIIA
Chicolla	ď	prev18232	164	CAGTGATATGATGCTGAACATCATCAACAGCTCTATTACTACCAAAGCCA1CA 365	SUMMENINSSITTMAISTW
	,			GCCGGTGGTCATCTTTGGCTTGCACATTGCCCTGGATGCTGTCAAGATGG1	SSLACINIALDAVRINIVARIEE
0.518.0				<u> ACAGTTTGAGGAGAATGGTCGGAAAGAGATTGACATAAAAAAATATGCAAGA</u>	NGHKEIDIKKYAHVEKIPGG
				GTGGAAAAGATACCTGGAGGCATCATTGAAGACTCCTGTGTCTTGCGTGGAG	IIEDSCVLRGVMINKDV I HP
				TCATGATTAACAAGGATGTGACCCATCCACGTATGCGGCGCTATATCAAGAA	RMRRYIKNPRIVLLDSSLEY
				CONTROL MANAGEMENT OF THE TOTAL GRANT ACADE A A A A A A A A A A A A A A A A A A	KKGGSQTDIEITREEDFTRI
				CAGACTGACATTGAGATTACACGAGAGGAGGACTTCACCCGAATTCTCCAGA	LOMEEEYIQQLCEDIIQLKP
				TO A CANCAL A CATCOLA CONTROL OF THE	DVVITEKGISDLAQHYLMRA
				CONTRACTOR TO A CARAGE GO CATCA CAGA TITAGE TO CAGE CATTAGE TO CAGA CATTAGA CA	NITAIRRVRKTDNNRIARAC
				**************************************	GARIVSRPEELREDDVGTG
				A LOCATED TO A CONTROLL OF THE TOTAL OF THE	AGLLEIKKIGDEYFTFITDCK
				CGCAI IGCI AGAGGCCCCCCCCCCCCCCCCCCCCCCCC	DPK
				AGAGAAGATGATGTTGGAACAGGAGCCIGIIGGAAAIIG	2 5
				GAGATGAATACTTTACTTTCATCACTGACTGCAAAGACCCCAAGGC	COCCUPATION OF THE PROPERTY OF
Shinella	œ	prev66739	165	ATGGACGACAAGGAGTTAATTGAATACTTTAAGTCTCAGATGAAAGAAGATCC 366	MDDKELIEYFKSQMKEDPU
o ollori	•			TGACATGGCCTCAGCAGTGGCTGCCATCCGGACGTTGCTGGAGTTCT1GAA	MASAVAAIRI LLEFLANDAG
0.6				A SA	ETIQGLRANLTSAIETLCGV
				CATACAAACCCTGTGTGTGTGTGTCCTCTGTGGCAGTGTCCTCTGGCGG	DSSVAVSSGGELFLRFISLA
				CALAGRACIO CONTROL CON	SLEYSDYSKCKKIMIERGEL
				THE STATE OF THE S	FLRRISLSRNKIADLCHTFIK
				CCAAA GI AAAAAGA CA	DGATIL THAYSRVVLRVLEA
				TATCACTGTCAAGAACAAAATTGCAGATCTGTCACCATCACCACCACCACCACCACCACCACCACCACCAC	AVAAKKBESVYVTESOPDI
				GGAGCGACAATATTGACTCACGCCTACTCCAGAGTGGTCCTCAGAGAGTCC	WENT OF THE WAY ON THE PROPERTY OF THE PROPERT
			_	GAAGCAGCCGTGGCGGCCAAGAAGCGATTTAGTGTACGTCACAGAGTCA	SGRAMMEN AND VIVOAR
				CAGCCTGATTTGTCAGGTAAGAAAATGGCCAAAGCCCTCIGCCACCICAACG	CONTRICT INTERVENTION OF
				TCCCTGTCACTGTGGTGCTAGATGCTGCTGTCGGCTACATCATGGAGAAAGC	GVVENGGIINKIGI NGINAV
			_	AGATCTTGTCATAGTTGGTGCTGAAGGAGTTGTTGAAAACGGAGGAATTATT	CAKACINKTTYVAESTRTV
		_		AACAAGATTGGAACCAACCAGATGGCTGTGTGTGCCAAAGCACAGAACAAAC	RLFPLNQQDVPDKFKYKAD
				CTTTCTATGTGGGTTGCAGAAAGTTTCAAGTTTGTCCGGCTCTTTCCACTAAAC	TLKVAQTGQDLKEEHPWV
				CAGCAAGACGTCCCAGATAAGTTTAAGTATAAGGCAGACACTCTCAAGGTCG	DYTAPSLITLLFTDL
				CGCAGACTGGACAAGACCTCAAAGAGGAGCATCCGTGGGTCGACTACACTG	
				CCCTTCCTTAATCACTCTGCTGTTTACAGACCTGGG	000
Shigella	9	prey67769	166	GCAGCCTTCAAGGTCGCCACGCCGTATTCCCTGTATGTCTGTC	AAFKVATPYSLYVCPEGUN
ipaH9.8				CAGAACGTCACCTCACCTGCAGGCTCTTGGGCCCTGTGGACAAAGAAAA	

TOOLERDY OILION

,		389 ARIKOLEALINSKEAALSTA LSEKATLEGELHDINGGVAR RUNDAENINGELDERINGGONENI RUNDAENINGELDERINGHEEDFO KNIYSEELRETKRHHETTRU V EIDNGKOHETESRI-JOALO ELRACHETOASHIETISIA OL VGAHELOOSHIETISIA OL EDSLARENDST SRRILLAEKE REMARINARMOOLUEY OLELUNIK JADMEHAYRIL LEGEERERIA SPSTYSORS RORLINGKA DIMEHAYRIL LEGEERERIA SPSTYSORS RORLINGKA DIMEHAYRIL LEGEERERIA SPSTYSORS RORLINGKA DIMEHAYRIL LEGEERERIA SPSTYSORS RORLINGKA DIMEHAYRIL LEGEERERIA SPSTYSORS RORLINGKA SP
GATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGGGGGCGAGGTGCAG ACCTGCTCAGAGCGCGGCCCATCGCAACCTCGAGGGGGCAGGACTTCAC CTGCACCAGGGCTGAGGCCCAACCCAA	COTTGGGGCTGGTCCTTTCAGCOLATGATAAAAACATAAAAACCTCC 388 COTCTGGATCCACCCCGGGGAACGGAACGGAACCTTAAAACATAAAAACATAAAACCTAAAAACCTAAAACCTAAAACCGGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACAAACGAACCAACGAACCAACGAACCAACCAACGAACGAACGAACCAACAACAACAAACAAACAAAA	SECCECAC TECATEMAT TECATEMAT TECATEMA AGACTECA GAACTECA GAACTECA GAACTECA GAACTECA GAACTECA GAACTECA GAACTECA GAACTECA GAACTCA CAACTCA CAACTCA CAACTCA CAACTCA CAACTCA CAACTCA CAACTCA CAACTCA
0400400FF4	167	90
	prey13613	prey/3837
	φ	ω
	Shigella paH9.8	Shigella paH9.8

FISHERY BELLER

				BEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	NGDDPLTYRFPKFTIKA GGWTUWAGAGATISPT DLWKAGNTWGCONSLH ALINSTGEEVAMRKLYRSV TVYEDDEDEDGDDLHHH HVSGSRR*
Shigella ipaH9.8	Ф	prey <i>67774</i>	8	TTGACTITGGGCCAATAATC 370 TTGACTITTCCTGTCAAG TTGACGTTTTTCCTGTCAAG TTGACGTAAG TTGACGTAAG TTGACGAGAGTGATAA TTGACGAGAGAGTGAAG TTGACGAGCATGAT TTGACGAGCATGAT AATTGACAACCACTTCAT AAATTGACAACCACTTCAT AAATTGACAATCATACAGA AAGGATTTCATCAGA AAGGATTTCATCAGA AAGGATTCATAAAC CCTTGACAACCATTCATAAC CCTTGACAATCATAAAC CCTTGACATCATAAAC CCTTGACATCATAAAC AAGGATTTCACACCATAAAC AAGGATTTTCACACCATAAAC AAGGATTTTCACACCATAAAC AAGGATTTTCACACCATAAAC AAGGATTTTCACACCATAAAC AAGGATTTTCACACCATAAAC AAGGATTTTCACACCATAAAC AAGGATTTTCACACCATAAAC CTCAGATGATTGCAATAAAC AAGGATTTTCACACCATAAAC CTCAGATGATTGCAATAAC CTCAGATGATTGCAATAAC AAGGATTAAACCTTAAAC CTCAGCAATAAAC CTCAGCAATAAAC CTCAGATGATTACACCATAAAC CTCAGCAATAAAC CTCAGCAACAACAACAACAACAACAACAACAACAACAACAAC	PPGERS,UFSGVYGPICQ PPGERS,UFSGVYGPICQ PSGPFCHTALEFOIL VSGHYORDERATITAL MFPCOWOHYVPLAGLHSNGLD DRSKLELDEDLAGFPKLEFV DRSKLELDEDLAGFPKLEFV DRSKLKRLPSELVSDK EELRYCLINGEPSENWLGFV GESSASKUKHLSSELVSDK RNGNINGSPLNSFELKEN FINALOGANICASTER EELRYCLINGESELVSDK EFRANDERANFT OMFADYERVYOCDE EELRYCLINGESPENSELK ENTRECANONINGENSENSE MFTNRECANONINGENSENSE BRONGKTTVDERENA GOGRYFEGFFFKLOMF GOGRYFEGFFFK GOGRYFEGFFFK GOGRYFEGFFF GOGRYFEGF GOGRYFEGFF GOGRYFEGFF GOGRYFEGFF GOGRYFEGFF GOGRYFEGFF GOGRYFEGFF GOGRYFEGF GOGRYFEGFF GOGRYFEGF GOGRYFE GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFEGF GOGRYFE GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGRYF GOGR
1	Q	27778 production 1977	170		WDSTKISKAYYKAMVISTW
Shigella ipaH9.8	٥	preyor r o	2	TTGGTGTTACTGGCTAAGAAAGAGGCACTTGATGCATGAAACAGACTCACGT	CYWLRKRHLMHETDSRVP

TODASHBY OSIOD

TTGGGCCAATTTGTTATCCATTTGAAAACATATNAAGTTTGATNCTAONTG ACAACGTNCTATNAAATGGGTGGGAGGTGGATNGGNCATGGGGTGTANAG GCGTGANGGCGG GGTGANGGCGG GGTCAGTGCTGGAGTCCACGGTGCCTCCAGCCACCTTGGG
ACCTICAGECATIONAL CONTROLL THE AGAITE AGGICGEAGCOST GEOGRA ACCTICAGECATIONAL CANAGE AGGICGEAGCT CANAGE TO AGAIN ACCAGEA ACCTICAGEACT CANAGEAGC AGGICT CANAGEA AGGICA AGGIC
COTGAGGACCAACCACATTGGGTGGGTGGGGTTTTGGGGTTTGGTGAAGAAAAAAA
GAGTANGGATCACCATTACTTTAAGTACTGCAAATCTCAGACATTGGACTTG TGAAGATGGTGATCACCATTACTTTAAGTACTGCAAATTCTGAAGATTGGACTTG TGAAGATGGTGATGCATCAGAAGACAATTTGGAAGTTATTGGACTGTGTGAAGAAGGTGATAATGCTGAATACTATTGAAGATTATTGGAATATGTTGAATACTATTGCAATATGATTGAATATGATTGAATACTATTGAATATGATTGAATACATTGAATACATTGAATACATTGAATACATTGAATACATTGAATACATTGAATACATTGAATACAATTGAATTGAATACATTGAATTGAATACATTGAATTGAATTGAATTGAATACAAGAATTGAATTGAATTGAATTTGATTGA

TOOTSTOY OLLLON

				GCTTGAGCTGTTGTGGAATAAATACTGGGTGAATACGTTGAGTTCTTCTAGCT TGCTTACTAATGC	N
Shigella	9	prey4060	174	GGCAAATCCTTTTCTTCAAAAAGGATTATAGTAAAGTCCAGCATCTGGCCC 375	ANHFFFKKDYSKVQHLALH AFHNTEVEAMQAESCYQL
ipaH9.8				TCAGCTAGCTAGATCATTCCATGTTCAGGAAGATTATGACCAAGCTTTTCAGT	ARSFHVQEDYDQAFQYYY
				ACTATTATCAAGCCACACAGTTTGCCTCATCCTCTTTTGTGCTCCCATTTTTG	QATQFASSSFVLPFFGLGQ
				GTTTGGGACAAATGTATATTTATCGAGGTGACAAAGAAAATGCATCTCAGTGC	MYIYRGDKENASQCFEKVL
				TTTGAGAAGGTTTTGAAAAGCTTATCCTAATAATTACGAAACIAIGAAAAIIUUC	SELUCINITE INICIASE I AC
				GGCTCTCTCTATGCTGCC CAGAAGA CAAGAAAAAACAAGA A GCCAAGA	QYPDDVEAWIELAQILEGT
				TO A A TTO GO A A A TOTTAGA A CAGACTGATATACAGGGTGCCCTTTCAGCC	DIQGALSAYGTATRILQEKV
				TATGGAACAGCAACACGAATCCTTCAGGAGAAAGTGCAGGCCGATGTTCCTC	QADVPPEILNNVGALHFRL
				CAGAGATTCTCAATAATGTGGGTGCCCTCCATTTTAGACTTGGAAACCTAGG	GNLGEAKKYFLASLDRAKA
				GGAGGCTAAGAAATATTTTTGGCGTCATTGGACCGTGCAAAAGCAGAAGCG	EAEHDEHYYNAISVIISYN
				GAACACGATGAGCATTACTATAACGCCATTTCCGTTACCACGTCATATAATCT	NII DELIBNIX/DCVI BI GAM
				CGCCAGGCTATATGAGGCGATGTGTGAATICCAIGAAGCAGAAAAACIGIAI	ADDIKONEYEASDWEKFAI
				AAAAACATCTTACGCGAACATCCTAATTATGIIGACIGCIAIIIGCGCCCIAGG	ANDRONAL LEASON I NEXT
				AGCCATGGCTAGAGATAAGGGAAACIIIIAIGAGGCICAGATIO	KOEWGDGOKKEEBII KOP
				GAAGCTCTTCAGATTAATCAGGATCATCCAGATGCTTGGICIIIGAIIGGCAA	STOSDIYSMI ALGNIXVI O
				TCTTCATTTGGCAAAACAAGAATGGGGICCIGGGCAGAAGAAGAIIIIGAGAAGG	TI HOPTBOBEKEKBHODB
				ATATTAAAACAGCCATCCACAGAGTGAIACCIAIGCIAIG	A AIYKOVI BNDAKNI YAA
				CAACGTGTGGCICCAAACIIIACAICAGCCAACGAAAAAAAAAA	NGIGAVI AHKGYEBEABDV
				AAGCGTCATCAAGA I CG I GC I C I GGCCA I C I ACAAACAAG I AC I CAGAAA I A	EACVBEATADISDVWI NI A
				ATGCAAAGAATCTGTATGC GCCAA GGCAA AGGAACC G I I I GGCCAACAA	HIX/EOKOXISA/OMYENG
				AGGATATTTCGTGAAGCTCGTGATGTAIIIGCCCAAGIAAGAAGCAACA	
	_			GCAGATATTAGTGATGTGTGGCTGAACTTAGCACACATCTATGTGGAGCAAA	LHKFTK
				AGCAGTACATCAGCGCCGTTCAGATGTATGAAAACTGCCTCCGAAAGTTCTA	
		V0000	175	CTCATCAACTACGGCTTCATCAACTACCTCTTCTATGGGGGCACGGTTG 376	LINYVGFINYLFYGGTVAGO
Shigella		prey49204	2	CTGGACAGATAGTCCTTCGCTGGAAGAAGCCTGATATCCCCCGCCCCATCAA	IVLRWKKPDIPRPIKINLLFPI
ранью				GATCAACCTGCTGTTCCCCATCATCTACTTGCTGTTCTGGGCCTTCCTGCTG	IYLLFWAFLLVFSLWSEPVV
				GTCTTCAGCCTGTGGTCAGAGCCGGTGGTGTGTGGCATTGGCCTGGCCATC	CGIGLAIMLTGVPVYFLGVY
	_			ATGCTGACAGGAGTGCCTGTCTATTTCCTGGGTGTTTACTGGCAACACAAGC	WOHKPKCFSUFIELLI LVS
				CCAAGTGTTTCAGTGACTTCATTGAGCTGCTAACCCTGGTGAGCCGAGAGAT	QKMCVVV ?PEVERGSGIE
				GTGTGTGGTCGTGTACCCCGAGGTGGAGCGGGGCTCAGGGACAGAGGAGG	EANEDWEEGGGCFW1GF1F
				CTAATGAGGACATGGAGGAGCAGCAGCACCCATGTACCAACCCACICCCA	בארטאלעתאלו
				_	I GI OA*ATAPG*VESAPFIE*
Shigella baH9.8	9	prey67686	176	CTGGGATTACAGGCATGAGCCACAGGACCIGGGIGAGITICICAGGAGGAGGATTATTGAAATAGAATAG	TVLSLVYVIAFVENEFTIDV*I

IDDATAS DILIDE

YEWULYYMSVFMLV PCCFGYYGSVV*SEVR*CD SSXFVLSAX FTOEDIDHAIAYLFPSGLFE KTARPVWKHPFOJFPRORA	IOWGEDGRPFHYLFYTGK QSYYSLMITSFTSRSHRTE NS* MEMRI PVARKPI SFRI GR	MEMILY TOTAL TOTAL DTKKHLVPGDTITTOTG ROSVERNIKLCWAL/TRTD GEVGDIVVGHTERRISAE GEVGDIVVGHTERRISAE GEVGDOVLVOVSPSLVKFQK KLGOGVLVOVSPSLVKFQK THFNLPCGASNICGNGF WIYPTEHKEEAGGFAN THFNLPCGASNICGNGF WIYPTEHKEEAGGFAN THPNLPCGASNICGNGF WIYPTEHKEEAGGFAN TOGNAMILYTOSILYCYEAS IPHONICOLIFYCHEAGGFAN TOGNAMILYTOSILYCYEAS IPHONICOLIFYCHEAGGFAN TOGNAMILYTOSILYCYEAS IPHONICOLIFYCHEAGGFAN TOGNAMILYTOSILYCYEAS IPHONICOLIFYCHEAGGFAN TOGNAMILYTOSILYCYEAS TOGNAMILYTOSILYCYEAS IPHONICOLIFYCHEAGGFAN TOGNAMILYTOSILYCYEAS TOGNAMILYCYEAS TOGNAMILYTOSILYCYEAS TOGNAMILYTOSILYCYEAS TOGNAMILYCYEAS TOGNAMILYTOSILYCYEAS TOGNAMILYCYEAS TOGNAMILYCY TOGNAMILYCYEAS TOGNAMILYCYEAS TOGNAMILY	RDLAMMYSCORKTVNEY RRCSSLERILRFLEDEMON EUVOLLEKSPLTPLPREM TLETVLEKELGELOGANON OOAKGSFLETTELKTLLKF TOPFFETETTEN ADDFFTED TSGLIELKKVDRAWTGKLG FIAGVINHERMASFERLLW RICHARUNTCKFSEMODRPLE DPVTKEETGKNIFITYOGE EPAVERREMESVNIPRED LITVITOTESHRGRLLOGA ANWHSWILKTOSKNIPRED
10 TC TC 378	3 8 8 8 8 8		AGG 380 380 380 380 380 380 380 380 380 380
AGITCACCATAGATGITGITAGATTIATTICTGGGTTCTCTATCCTGTTCTGTT	TGITTGAGAAQGAGGCAGGCAGTAA IGAAGATU LU INOV AQQACAAGAGGCATTCGGTGGGGAGAAGATGGCCGTCCATTTGACTATOT TTGATACTGGCAAACAGTCATTGATTACTATGATTACCAGCTTTACTTGC CGATCACACAGGAGAGAGGCTGA	ATGGARATIGAGGETCOLAGETCGGARGACTOTT AGGGARGARA, UGBGA GGGGACACTAGAAACATCTAGTGGTCGCGGGGGATTACATACATACATACATTACATTACATTACATA	CAMAGATTIAAATATGAATGTGAAGGCTTTGAAGGAAATTIGTGAAGAAGATTTGTGAAGAAGGAAG
177		178	179
prey66872		prey67690	prey67695
9		ω	ω
Shigella	іраН9.8	Shigella ipaH9.8	Shigella ipaH9.8

10043487.01110

				DIAMETAN COOP (CITACON)
			TCACCGCCAGCGCCTGCTGCAGGAAGCCGCTGCCAACTGGCACTCCTGGCI	VADATRIKRALEGGMELSG
				SSMAPIMTTVQSKTAPPTF
			GATGCCACACGTATCAAGAGGGCACTGGAGCAAGGCATGGAACTAAGTGGC	<u></u>
			TCCTCCATGGCCCCCATCATGACCACAGTGCAATCTAAAACAGCCCCTCCCA CATTTAACAGGAC	
Shiqella 6	prey67336	180	ATGGGAGTGACATGGGACTTCAGCATGAGCAATGGAGGGCCCCGTGGGGAA 381	MGVTWDFSMSNGGPRGK
lipaH9.8			GACCTATGCTTTCAAGGGGGACTATGTGTGGACTGIAICAGAIICAGGACCG	TATKED I WAT VSDSGT IS
	-		GGCCCCTTGTTCCGAGTGTCTGCCCTTTGGGAGGGGCCICCCCGGAAACCIG	VYSEPTOWIHEEKSDKVW
			GATGCTGCTGTCTACTCGCCICGAACACAAIGGAIICACIICIIIAAGGGAAG	OVINEYMSDGEBKKI NBVE
			ACAAGGTGTGGCGCTACATTTAATTTCAAGATGTCTCCTGGCTTCCAAGAA	DAM DAM YAZIBI NOKYELEK
			GCTGAATAGGGTAGAACCTAACCTGGATGCAGCICICIAIIGGCCICICAAC	GSGYWQWDFI ABTDESSY
			CAAAAGG	PKPIKGLFTGVPNOPSAAM
			GCCCGAACTGACTTCGCCTGCTGCTATGCGCTTGCCAAGATGGCCGAGGTCT	SWQDGRVYFFKGKVYWRL
			A CONTROL A A GOOD ON A A GOOD ON A A GOOD ON A GOOD ON A GOOD ON A A GOOD ON A A GOOD ON A GOOD	NQQLRVEKGYPRNISHNW
			AN AND DOTATION AND ATAITING CONCADANCIAGA TO CONTAIN AND AN ANA ANA ANA TAITING CAN AND AN ANA TAITING CONCADANCIAGA TO CONTAIN AND ANA TAITING CONCADANCIAGA TO CONTAIN AND AN ANA TAITING CONCADANCIAGA TO CONTAIN AND AN AND AND AND AND AND AND AND AND	MHCRPRTIDTTPSGGNTTP
			ACTATAGACACTACCCCATCAGGTGGGAATACCACTCCCTCAGGTACGGGCA	SGTGITLDTTLSATETTFEY*
			TAACCTTGGATACCACTCTCTCAGCCACAAACCACGTTTGAATACTGA	
on called	0009000	ă	AGACCAGAGCCATGTTCTAAGAGCATTTAAGTGAAGAAAGGATGAAAGA 382	DOSHVVQEHLSEEKDERL
Suigella	preyozaa	2	CTACACTGTGAGAATAATGATAAAGCCCCTGAATCAGAGTCAGAGAGAG	HCENNDKAPESESEKPTPL
pana.o			CTCCTCTGTCCACTGGGCAAGGTAATAGAGCTGAAGAGGGACCAAACGCTA	STGGGNRAEEGPNASSGF
			GTTCAGGTTTCATGAAGACTGCTGTACTAGGACCTACACTGAAAAATGTAATG	MKTAVLGPTLKNVMMKNN
			ATGAAAAATAAAACTAGCAGTTTCCCCTAACTATAATGCTACGTTTATGG	KLAVSPNYNATFMGFKMM
_			CTTCAAGATGATGGAAAACAGCATATTGTATTAAAATTGGTGCCTATCA	DGKQHIVLKLVPIKQNVCSP
			AACAAAATGTATGTTCACCAGGCTCACAGTCAGGTGCTGCAAAGGACGGTAC	GSQSGAAKDGTANLQPQT
			TGCTAATTTGCAGCCCCAGACTTTGGACACTAATGGATTTTTAACAGGAGTAA	LDTNGFLTGVTTELNDTVY
			CAACTGAGTTAAATGACACAGTTTATATGAAAGCAGCTACTCCATTTTCATGT	MKAATPFSCSSSILSGKAS
			TCATCTTCTATACTTTCAGGGAAAGCAAGTTCAGAAAAAAAA	SEKEMILISORNAMICIAND
			ATCTCAAAGGAATAATATGCTTCAAACAATGGATTATGAGAAAAGTGTATCTI	YEKSVSSLSA I SELVI ASV
			CTTTGTCAGCAACATCAGAATTGGTTACAGCATCAGTGAATTTGACCACAAAA	NEI IKFEI RUNVUTWGNAL
			TTTGAAACAAGAGATAATGTTGACTTCTGGGGAAATCATCTCACTCA	TOSHPEVLGTTIKSPDKVN
		_	CCCCGAGGTATTAGGTACCACCATTAAAAGTCCAGATAAAGTCAACTGTGT	CVARPINATINSGDIMINTOL
			GCCAAACCAAATGCATACAACAGTGGAGATATGCATAATTATTGCATTAATTA	NYGNCELPVESSNGGSLPF
			TGGCAACTGTGAGTTACCTGTTGAATCCTCCAACCAAGGATCATTACCTTTC	C/VTXISSSSSSCORTXVX
			ATAATTACTCAAAAGTGAATAATTCTAATAAACGTCG1AGG1111CAGGAACA	AV TENTONESSON I VVO
			GCAGTGTATGAAAACCCTCAAAGAGAAICIICAICCAGCAAAACAGIIGIUU	GPISESPESEVICACIONI DE SILI ASISI I NOKOGTI KAKS
			AACAACCAATTAGTGAATCATTTACACTAGTGAGGCAGGAGAGCTTTTAAAATGATAAAGATGGAACTTT	FIFEDYVLEKGONIDGONL
			CCAGAIAGCOIAIIAGCAICIAIIAGCOIII	

IDD43487.011102

	-		ľ		YSNENONLECATEKSKWE	ATEKSKWE
				AAAAGGAAAA DOOTGAAGAAA TAAAAAAAAAAAAAAAAAAAAAAAAAAAA	DESNVDSPMMPRITSVFSL	APRITSVFSL
				GAAAAATCTAAATGGGAAGACTTTTCTAATGTCGATTCACCTATGATGCCTAG	QSQQASEFLPPEVNQLLQD	PEVNOLLOD
	_			A A TO A CATOTIC TOTO TOTO COA GOOD A GOOD TO CAGA A TOTO TOTO TOTO TOTO TOTO TOTO TOTO	VLKIKPDVKQDSSNTPNKG	SSNTPNKG
	_		_	CTGAAGTAAACCAATTGCTTCAGGATGTATTGAAAATAAAACCTGATGTAAAA	LPLHCDQSFQKHEREGKIV	KHEREGKIV
	_			CAACACTCTAGTAGCACTCCAAATAAAGGCTTGCCACTTCATTGTGACCAGTC	ESSKDFKVQGIFPVPPGSV	IFPVPPGSV
				ATTICA A A A A A A CONTRACTOR A	GINVPTNDLNLKFGKEKQV	-KFGKEKQV
				A A PARA A A B B B B B B B B B B B B B B B B	SSIPQDVRDSEKMPRISGF	EKMPRISGF
				TACABATGATTTGAATTTGAAATTTGGAAAAGAAAAAAAAGAAAAGTGTCATCAATAC	GTLLKTQSDAIITQQLVKDK	ITQQLVKDK
				CACAAGATGTGAGAGATTCAGAGAGATGCCTAGAATTTCAGGTTTTGGCAC	LRATTQNLGSFYMQSPLLN	FYMOSPLLN
				ATTACTTAAGACTCAGTCAGATGCGATAATAACACAGCAGCTTGTAAAAGACA	SEQKKTIIVQTSKGFLIPLNI	SKGFLIPLNI
				A A CTA C SA G C A C C A C C A C A C A C A C A C A	TNKPGLPVIPGNALPLVNS	SNALPLVNS
			•	TTABATTCAGAACAAAAAAAAAACTATAATTGTTCAGACTTCAAAAAGGATTCTTA	QGIPASLFVNKKPGMVLTL	KKPGMVLTL
				ATACCATTGAACATTACTAACAAGCCTGGGCTACCAGTTATTCCTGGAAATGC	NNGKLEGVSAVKTEGAPA	VKTEGAPA
	_			ACTTCCATTGGTTAATTCACAAGGTATCCCTGCTTCTTTTTGTAAACAAGAA	RGTVTKEPCKTPILKVEPN	TPILKVEPN
			_	A C C T G G G A T G G T T T T A A C A C T T A A T A G G A A A C T T G A A G G T G T T C C G C T	NNCLTPGLCSSIGSCLSMK	SIGSCLSMK
				GECAAAACOGAGGEGGCCCAGCTCGTGGAACTGTGACTAAGGAGCCTTGC	SSSENTLPLKGPYILKPTSS	GPYILKPTSS
				AAAACACCTATTTTGAAGGTAGAACCAAACAATAATTGTCTTACACCTGGACT	VKAVLIPNMLSEQQSTKLNI	SEGGSTKLNI
				TTGTTCCAGCATTGGCAGTTGTTTGAGCATGAAAAGTAGCTCAGAAAATACTT	SDSVKQQNEIFPKPPLYTFL	FPKPPLYTFL
				TECCATTAAAAAGGCCCTTACATTTTGAAACCAACGAGTTCTGTGAAAGCTGTT	PDGKQAVFLK	PDGKQAVFLKCVMPNKTEL
				CTTATTCCTAACATGCTATCTGAGCAACAGAGCACTAAGTTGAATATCTCCGA	LKPKLVQNSTYQNIQPKKP	YQNIQPKKP
				TTCAGE AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	EGTPQRILLKIFNPVLNVTA	FNPVLNVTA
				COTTO TO THE TANA A SECTION TO THE TANA A STORY OF THE TANA A STOR	ANNLSVSNSA	ANNLSVSNSASSLOKDNVP
				AGCTGCTTAAGCCCAAATTAGTCCAAAATAGTACTTATCAAAATACAGCCA	SNQIIGGEOKEPESRDALP	EPESRDALP
	_			AAGAAACCTGAAGGAACACCACAAAGAATATTGCTGAAAATTTTTAACCCTGT	FLLDDLMPANEIVITSTATC	EIVITSTATC
				TTTAAATGTGGTGCTGCTAATAATCTGTCAGTAAGCAACTCTGCATCCTCAT	PESSEEPICVSDCSESRVL	SDCSESRVL
				TGCAAAAAGACGAACGTACCATCTAATCAGATTATAGGAGGAGAGAGA	RCKTNCRIERNFNRKKTSK	NFNRKKTSK
				GCCAGAATCTAGAGATGCCTTACCCTTACTAGATGACTTAATGCCAGCAA	KNFFKNKNSWK*	VK*
				ATGAAATTGTGATAACTTCTACTGCAACATGCCCAGAATCTTCTGAGGAACCA		
				ATATGTGTCAGTGACTGTTCAGAGTCCAGGGTATTAAGGTGTAAAACAAATTG		
				TAGAATTGAGAGGAACTTCAATAGAAAAAAGACTTCCAAAAAAAA		
				AAACAAAAACTCATGGAAGTAA		
Shigella 6		prey6586	182	CGCGCCGTGGAAGAAGATCCAGCAGAACACTTTCACGCGCTGGTGCAACGA 383	APWKKIQQNTFTHWCNEP	APWKKIQQNTFTHWCNEH
ipaH9.8	-			GCACCI GAAG I GCG I GAGCAAGCGCAI CGCCAAGCI CGCCAAGCI CGCAAGCAAGAAGAAT	RI IAI I FVI SC	BI IAI I FVI SOKKMHRKHN
_				CGACGGGC GCGGC IA CGCGC GTTTTCGCCAAATGCAGCTTGAGAA	ORPTFROMO	ORPTFROMOLENVSVALEF
				SOTOTO CONTROL ACTION OF THE CONTROL	LDRESIKLVSI	LDRESIKLVSIDSKAIVDGNL
				CATCGACAGGAAGGCCATCGTGGACGGGAACCTGAAGCTGATCCTGGGCCT	KLILGLIWTLII	KLILGLIWTLILHYSISMPMW
				CATCHEGACCCTGATCCTGCACTACTCCATCCCATGCCCATGTGGGACGAG	DEEEDEEAK	DEEEDEEAKKOTPKORLLG

GTYIVTITWGGQNIGRSPFE VKVGTECGNOKVRAWGPG MADIRDAPQDFHPDRVKAR KVKVYGPGVAKTGLKAHEP GVELGKPTHFTVNAKAAGK KTTYFEIFTAGAGTGEVEVV KGVRVKETADFKVYTKGAG GPGLEKTGVAVNKPAEFTV SYVPRKPVKHTAMVSWGG NONDIFTVKYTPRGAGSYT **IMVLFADQATPTSPIRVKVE** SGRALGALVDSCAPGLCPD QQADDWLGIPQVITPEEIVD SVWYVPEVTGTHKVTVLFA GOHIAKSPFEVYVDKSQGD ASKVTAQGPGLEPSGNIAN GOACNPSACRAVGRGLOP DAKHGGKAPLRVQVQDNE VSIPNSPFRVNVGAGSHPN WICHKI POL PITNESRDWO **PNVDEHSVMTYLSQFPKAK SPGIEPTGNMVKKRAEFTV** OKDLGDGVYGFEYYPMVP I EGGVVGKSADFVVEAIGD DVGTLGFSVEGPSQAKIEC TYFTVDCAEAGQGDVSIGI KCAPGVVGPAEADIDFDIIR WDSWDASKPVTNAREAM LKPGAPLRPKLNPKKARAY GHOFFAKVTANNDKNRTF IQDPMGQKGTVEPQLEAR BDSTYRCSYOPTMEGVHT VHVTFAGVPIPRSPYTVTV SGELKVTVKGPKGEERVK DDKGDGSCDVRYWPQEA GEYAVHVLCNSEDIRLSPF GCPVEALVKDNGNGTYSC PSHDASKVKAEGPGLSRT ETRSAGGEVLVYVEDPA GTGCGGGTGAAGGAGACAGCTGACTTCAAGGTGTACACAAAGGGCGCTGGC A C G G G C C T G G G C C T G G G C G G C G T T G G C A G T C A G TGGATGCCAAGCACGGTGGCAAGGCCCCACTTCGGGTCCAAGTCCAGGACA GCTGGCAGCCACCCAACAAGGTCAAAGTATACGGCCCCGGAGTAGCCAAG ACAGGGCTCAAGGCCCACGAGGCCCACCTACTTCACTGTGGACTGCGCCGAG GTAACCCGAGTGCCTGCCGGGCGGTTGGCCGGGGCCTCCAGCCCAAGGGT AGTGGGGAGCTGAAGGTCACCGTGAAGGGCCCCCAAGGGAGGAGGGGCGCGT GCGCAGTCCCTTCGAAGTGAAGGTGGGCACCGAGTGTGGCAATCAGAAGGT CTCCTGTGATGTGCGCTACTGGCCGCAGGAGGCTGGCGAGTATGCCGTTCA CTGGATTGGAGAAGACAGGTGTGGCCGTCAACAAGCCAGCAGAGTTCACAG ATGAAGGCTGCCCTGTGGAGGCGTTGGTCAAGGACAACGGCAATGGCACTT AGCCCACAGGCAACATGGTGAAGAAGCGGGCAGAGTTCACTGTGGAGACCA CAGTGGCAACATCGCCAACAAGACCACCTACTTTGAGATCTTTACGGCAGGA GCAGCTACCAGCCCACCATGGAGGGCGTCCACACCGTGCACGTCACGTTTG GAAGCAGAAGGACCTGGGGGATGGCGTGTATGGCTTCGAGTATTACCCCAT CCGTGACGCGCCCCAGGACTTCCACCCAGACAGGGTGAAGGCACGTGGGC ACAGCTGCTCCTACGTGCCCAGGAAGCCGGTGAAGCACACAGCCATGGTGT GCTGGCCAGGGGGACGTCAGCATCGGCATCAAGTGTGCCCCTGGAGTGGT GAGGAGGATGAGGAGGCCAAGAAGCAGACCCCCAAGCAGAGGCTCCTGGG CTGGATCCAGAACAAGCTGCCGCAGCTGCCCATCACCAACTTCAGCCGGGA GGCCTGTGTCCTGACTGGGACTCTTGGGACGCCAGCAAGCCCGTTACCAAT GCGCGAGAGGCCATGCAGCAGGCGGATGACTGGCTGGGCATCCCCCAGGT CACCAGGAGGAGGCAAAAGTGACCGCCAATAACGACAAGAACCGCACCTTC rccetctegtacetcccceaegtgaccegegactcataaggttactgtgctc TTTGCTGGCCAGCACATCGCCAAGAGCCCCTTCGAGGTGTACGTGGATAAG GCTGGCACGGGCGAGGTCGAGGTTGTGATCCAGGACCCCATGGGACAGAA GGGCACGGTAGAGCCTCAGCTGGAGGCCCGGGGCGACAGCACATACCGCT CCGGCGTGCCCATCCCTCGCAGCCCCTACACTGTCACTGTTGGCCAAGCCT GGTCCCTGGAACCTATATCGTCACCATCACGTGGGGTGGTCAGAACATCGG ACTITIGIGGIGGAGGCTATCGGGGACGACGTGGGCACGCTGGGCTTCTCG GTGGAAGGGCCATCGCAGGCTAAGATCGAATGTGACGACAAGGGCGACGG CGTGCTGTGCAACAGCGAAGACATCCGCCTCAGCCCCTTCATGGCTGACAT CCTGGGGAGGCGTCAGCATCCCCAACAGCCCCTTCAGGGTGAATGTGGGA GATCACCCCGAGGAGATTGTGGACCCCAACGTGGACGAGCACTCTGTCAT TCACAGGGTGACGCCAGCAAAGTGACAGCCCAAGGTCCCGGCCTGGAGCC CTGGCAGAGCGGCCCGGGCCCTGGGCGCCTGGTGGACAGCTGTGCCCCG GACCTACCTGTCCCAGTTCCCCAAGGCCAAGCTGAAGCCAGGGGCTCCCTT GCGCCCAAACTGAACCCGAAAAAGCCCGTGCCTACGGGCCAGGCATCG

FTVETRGAGTGGLGLAVEG DASKVKASGPGLNTTGVPA SPVPSSPFQVPVTEGCDPS RVRVHGPGIQSGTTNKPNK QVPGSPFKVPVHDVTDASK QSFQVDTSKAGVAPLQVKV YGDEEVPRSPFKVKVLPTH SLPVEFTIDAKDAGEGLLAV YGGDEIPFSPYRVRAVPTG LECLDNGDGTCSVSYVPTE VEYTPYEEGLHSVDVTYDG QITDPEGKPKKTHIQDNHD GTYTVAYVPDVTGRYTILIK VDIIDHHDNTYTVKYTPVQQ SVAVSPSLDLSKIKVSGLGE GOGKVASKIVGPSGAAVPC KVEPGLGADNSVVRFLPRE GAYTVTIKYGGOPVPNFPS GIEGGGVFREATTEFSVDA SGNLTETYVQDRGDGMYK PSEAKMSCMDNKDGSCSV **EYIPYEAGTYSLNVTYGGH** VKCSGPGLSPGMVRANLP **QGPKGLVEPVDVVDNADG** TOTVNYVPSREGPYSISVL PGLQGGSAGSPARFTIDTK GLERATAGEVGQFQVDCS VYIQDHGDGTHTITYIPLCP RALTQTGGPHVKARVANP GKLDVQFSGLTKGDAVRD GPVGVNVTYGGDPIPKSPF KVDVGKDQEFTVKSKGAG EGPYEVEVTYDGVPVPGS PEPI FAVAPTKPSKVKAFG GAGTGGLGLTVEGPCEAQ PGDYNINILFADTHIPGSPF KAHVVPCFDASKVKCSGP SAGSAELTIEICSEAGLPAE KI QVEPAVDTSGVQCYGP CTTACGAGGAGGACTGCACTCCGTGGACGTGACCTATGACGGCAGTCCCG TCAACGTCACCTATGGTGGCCATCAAGTGCCAGGCAGTCCTTTCAAGGTCCC FIGGAGGGGATCCCATCCCTAAGAGCCCTTTCTCAGTGGCAGTATCTCCAAGC TGAAGGCGTTTGGGCCGGGGCTGCAGGGAGGCAGTGCGGGCTCCCCCGCC ATTCCCCTCTGCCCCGGGGCCTACACCGTCACCATCAAGTACGGCGGCCAG TGGCTGTAGAGGGCCCCTCCGAGGCCAAGATGTCCTGCATGGATAACAAGG TGTGCATGATGTGACAGATGCGTCCAAGGTCAAGTGCTCTGGGCCCGGCCT SAGCCCAGGCATGGTTCGTGCCAACCTCCCTCAGTCCTTCCAGGTGGACAC CAGTCAAGTACACGCCTGTCCAGCAGGGTCCAGTAGGCGTCAATGTCACTTA AAAGTGGCATCCAAGATTGTGGGCCCCTCGGGTGCAGCGGTGCCCTGCAAG CTGGCAGCCCTTTCCTCTGGAAGCTGTGGCCCCCCACCAAGGCCTAGCAAGG GGTGGAGGCCCCTGTGAGGCGCAGCTCGAGTGCTTGGACAATGGGGATG ACATCCTCTTCGCTGACACCCACATCCCTGGCTCCCCATTCAAGGCCCACGT GCGGGCCACCGCTGGGGAGGTGGGCCAATTCCAAGTGGACTGCTCGAGCG CGGGCAGCGCGGAGCTGACCATTGAGATCTGCTCGGAGGCGGGGGCTTCCG CCCGTGCCCAACTTCCCCAGCAAGCTGCAGGTGGAACCTGCGGTGGACACT TCCGGTGTCCAGTGCTATGGGCCTGGTATTGAGGGCCAGGGTGTCTTCCGT AGGGCCGCACGTCAAGGCCCGTGTGGCCAACCCTCAGGCAACCTGACGG AGACCTACGTTCAGGACCGTGGCGATGGCATGTACAAAGTGGAGTACACGC CAACAAGTTCACTGTGGAGACCAGGGGAGCTGGCACGGGCGGCGTGGGCC CTGGACCTCAGCAAGATCAAGGTGTCTGGCCTGGGAGAGAAGGTGGACGTT GGCAAAGACCAGGAGTTCACAGTCAAATCAAAGGGTGCTGGTGGTCAAGGC GTGGAGCCAGGCCTGGGGGCTGACAACAGTGTGGTGCGCTTCCTGCCCCG GCACATGTTCCGTGTCCTACGTGCCCACCGAGCCCGGGGGACTACAACATCA GGTTCCCTGCTTTGACGCATCCAAAGTCAAGTGCTCAGGCCCCGGGCTGGA GCCGAGGTGTACATCCAGGACCACGGTGATGGCACGCACCATTACCTAC GAGGCCACCACTGAGTTCAGTGTGGACGCCCGGGCTCTGACACAGACCGG TGCCCAGCAGCCCCTTCCAGGTGCCCGTGACCGAGGGCTGCGACCCCTCC CGGGTGCGTGTCCACGGGCCAGGCATCCAAAGTGGCACCACCAACAAGCC AAGCTGCTGGCAAAGGCAAGCTGGACGTCCAGTTCTCAGGACTCACCAAGG TGAGGAAGGGCCCTATGAGGTGGAGGTGACCTATGACGGCGTGCCCGTGC CGCTTCACCATCGACACCAAGGGCGCCGGCACAGGTGGCCTGGGCCTGAC CACCTTCACGGTCAAGTACACGCCCCGGGGGGGCTGGCAGCTACATTAT GGTCCTCTTTGCTGACCAGGCCACGCCCACCAGCCCCATCCGAGTCAAGGT GTCGCACTGGTGTCGAGCTTGGCAAGCCCACCCACTTCACAGTAAATGCCA AGGCCCGCCGAAGCTGACATCGACTTCGACATCATCCGCAATGACAATGA GGAGCCCTCTCATGACGCCAGTAAGGTGAAGGCCGAGGGCCCTGGCCTCA

OSEIGDASRVRVSGQGLHE KFADQHVPGSPFSVKVTGE **AEAGVPAEFSIWTREAGAG** SPSGDARRLTVSSLQESGL QQLAPQYTYAQGGQQTWA SYAPSFAGI HEMDIRYDNM GRVKESITRRRAPSVANV GLAIAVEGPSKAEISFEDRK **HIPGSPLQFYVDYVNCGHV** TAYGPGLTHGVVNKPATFT GSPETARVTGDDSMRMSH RNGHVGISFVPKETGEHLV GI SI SIEGPSKVDINTEDLE DGTCRVTYCPTEPGNYIINI QVTSPSGKTHEAEIVEGEN HTYCIRFVPAEMGTHTVSV KYKGQHVPGSPFQFTVGP LGEGGAHKVRAGGPGLER DGSCGVAYVVQEPGDYEV KVNQPASFAVSLNGAKGAI DASKCTVTVSIGGHGLGAG GPTIQIGEETVITVDTKAAG DVVENEDGTFDIFYTAPQP GKYVICVRFGGEHVPNSPF PERPLYGYNGLDVTSLRPF SGKVAQPTITDNKDGTVTV VNTKDAGEGGLSLAIEGPS KAEISCTDNQDGTCSVSYL PVLPGDYSILVKYNEQHVP LKVGSAADIPINISETDLSLL **FATVVPPSGREEPCLLKRL** GSHCDLSLKIPEISIQDMTA SVKFNEEHIPDSPFVVPVA DAKVHSPSGALEECYVTEI KGKVTCTVCTPDGSEVDV QVTALAGDQPSVQPPLRS OI VIPFTIKKGEITGEVRMP HVKKNGQHVASSPIPVVIS GHTFEPAEFIIDTRDAGYG CTGCGTAATGGCCACGTGGGGATTTCATTCGTGCCCAAGGAGACGGGGGAG CAATGGGCTGGATGTGACCAGCCTGAGGCCCTTTGACCTTGTCATCCCCTTC GATGGGACATGCAGCGTGTCCTACCTGCCTGTGCTGCCGGGGGACTACAGC CCGGTGGTGATCAGCCAGTCGGAAATTGGGGATGCCAGTCGTGTTCGGGTC TCTGGTCAGGGCCTTCACGAAGGCCACACCTTTGAGCCTGCAGAGTTTATCA TTGATACCCGCGATGCAGGCTATGGTGGGCTCAGCCTGTCCATTGAGGGCC CAATTATGTGCCCAGCCGAGAAGGGCCCTACAGCATCTCAGTACTGTATGGA AGGGCCTGCTGGCTGTCCAGATCACGGATCCCGAAGGCAAGCCGAAGAAGA rgcactgtcacagtgtcaatcggaggtcacgggctaggtgctggcatcggc GCAGGCAAAGGCAAAGTGACGTGCACCGTGTGCACGCCTGATGGCTCAGAG ACGGCCCCCAGCCGGGCAAATACGTCATCTGTGTGCGCTTTGGTGGCGAG ACCATCAAGAAGGGCGAGATCACAGGGGAGGTTCGGATGCCCTCAGGCAAG GTATGCACCCAGCGAGGCTGGCCTGCACGAGATGGACATCCGCTATGACAA CCTGCCACCTTCACCGTCAACACCAAGGATGCAGGAGAGGGGGGCCTGTCT ATTCTAGTCAAGTACAATGAACAGCACGTCCCAGGCAGCCCCTTCACTGCTC GGGTCACAGGTGACGACTCCATGCGTATGTCCCACCTAAAGGTCGGCTCTG CCACTGTGGTCCCGCCCTCGGGCCGGGAGGAGCCCTGTTTGCTGAAGCGG CACCTGGTGCATGTGAAGAAAATGGCCAGCACGTGGCCAGCAGCCCATC CCAGCAAGGTGGACATCAACACAGAGGACCTGGAGGACGGGACGTGCAGG GTCACCTACTGCCCCACAGAGCCAGGCAACTACATCATCAACATCAAGTTTG AAGCAAGGCTGGTGTGGCCCCATTGCAGGTCAAAGTGCAAGGGCCCAAAGG CCTGGTGGAGCCAGTGGACGTGGTAGACAACGCTGATGGCACCCAGACCGT CCCACCATTCAGATTGGGGAGGAGGACGGTGATCACTGTGGACACTAAGGCG GTGGATGTGGACGTGGTGGAGAATGAGGACGGCACTTTCGACATCTTCTAC TCGGTGCAGCCCCCTCTACGGTCTCAGCAGCTGGCCCCACAGTACACCTAC CATGCACATCCCAGGAAGCCCCTTGCAGTTCTATGTGGATTACGTCAACTGT GGCCATGTCACTGCCTATGGGCCTGGCCTCACCCATGGAGTAGTGAACAAG CTGGCCATTGAGGGCCCGTCCAAAGCAGAAATCAGCTGCACTGACAACCAG CTGCCGACATCCCCATCAACATCTCAGAGACGGATCTCAGCCTGCTGACGG CCGACCAGCACGTGCCTGGCAGCCCCTTCTCTGTGAAGGTGACAGGCGAG CCTTCTCCCCGTACCGCGTGCGTGCCGTGCCCACCGGGGACGCCAGCAAG GATGAAGAGGTACCCCGGGAGCCCCTTCAAGGTCAAGGTGCTGCCTACTCAT GCCTGCCAGCCTGCCCGTGGAGTTCACCATCGATGCAAAGGACGCCGGGG CACACATCCAAGACAACCATGACGGCACGTATACAGTGGCCTACGTGCCAG ACGTGACAGGTCGCTACACCATCCTCATCAAGTACGGTGGTGACGAGATCC GTGGCGCAGCCACCATCACTGACAACAAAGACGGCACCGTGACCGTGCG GATGCCAGCAAGGTGAAGGCCAGTGGCCCCGGGGCTCAACACCACTGGCGT

and the second s

COCOTGAATT AGCATT COCOTGAATT AGCATT COCOTGAATT AGCATT COCOTTGAATT AGCATT COCOTTGAATT AGCATT COCOTTGAATT AGCATT COCOTTGAATT AGCATT COCOTTGAATT AGCATT COCOTGAATT AGCATT COCOTGAATT AGCATT COCOTGAAT AGCAT		POSCTATTTGGGGACACT 384 ACTGGACGGATGTGCCC WCOVAGNUDRFHTFPRLA ACAGACTTCACTTGCACT GGGGCACTCCGGTGCC WCOVAGNUDRFHTFPRLA GGGACCCCCCCGCCAGC SACSRLYAPASLAVPHSLAVPGGCAC SACSRLYAPPSLAVPOKGRA SACSRLYAPPSLAVPOKGRA SACSRLYAPPSLAVPOKGRA
GGCCGGGTGAAAGAAGATCACCCGCAGGCGTCGGGGCTCCTTCAGTGGC CANCOTTGGTAGTTGTGACCTCAGCCTGAAATCCCTTAAATTAGAAT CAGGATATGACCAGCTGACCTGAC	ACGGCTCCTGTGGTGGTGGTGGTGGTGTGTGTGTGTGCGTGGTG	
		18
		prey56789
		_o
		Shigella ipaH9.8

TISTER INTERIOR

			ľ	CATTEATECCAAGTCCTTTGCCCGTATCAAGAAGTGGCTGGAGCACGCGCG	ARSSPSLTILAGGKCDDSV
				CICTOGOCOGÓCICACOATCCTGGCTGGGGGCAAGTGTGATGACTCGT	GYFVEPCIVESKDPQEPIM KEEIFGPVLSVYVYPDDKY
				CATCATGAAGGAGGAGATCTTCGGGCCTGTACTGTCTGTGTACGTCTACCCG	KETLQLVDSTTSYGLTGAV
				GACGACAAGTACAAGGAGACGCTGCAGCTGGTTGACAGCACCACCAGCTAT	FSQDKDVVQEATKVLHNAA
				GGCCTCACGGGGGGCAGTGTTCTCCCCAGGATAAGGACGTCGTGGTGGAGGAGGC	GNFYINDKSIGSIVGGGFF
				CACAAAGGTGCTGAGGAATGCTGCCGGCAACIICIACAICAACGACAACAGGICC	BWTSPOVIKETHKPLGDW
				ACTGGCTCGATAGIGGGCCAGCCCIIIGGGGGGGCCCGAAGCCICIGG	SYAYMO*
				AACCAATGACAAGGAGACACATAAGCCCCTGGGGGACTGGAGCTACGCGTA	
Shinella	œ	prev67711	184	AACAGAGCTGCCTCCTGGCTCTTTGGGAGCCTGGGAGGAGGAGGAGGCCGG 385	NRAASWLFGSLGGEGAGH
inaH9.8				GAGGGGCGCTGCGGGGAAGCCACCTGCGGATTCACTGGCTGCTGCTGCTCCGC	GAAGKPADSLAAAPPRIA
2				CCAGGACTGCTAGCAAGCACGGAGGGCTGCCAGACCTGGGGGCTCCCTGCT	SKHGGLPDLGLPAPCVRLG
				CCGTGCGTCAGGTTGGGGAAACCACCGTCTGCCCCAGACCCTGACCCAGGA	KFFSAFDFDFGFAWDK
				CCCGCC I GGAGGAGGC GGG	MSOAVOTNGTOPI SKTWF
Shigella	9	prey2118	185		I SI YEI OBTROFAITDGLEI
ipaH9.8				AACI CAGII I AI AI GAGII ACAACGAACACO CAGGAACACACACACACACACACACACACACACACACAC	VVSPRSLHSELMCPICLDM
				CITAGAAAI IGIGGII I I CACCI CGAAGI CIACACAGI GACACAGI ACACACAGI GACACAGI ACACACAGI ACACACAGI ACACACAGI ACACACAGI ACACACAGI ACACACAGI ACACACAGI ACACACAGI ACACACACAGI ACACACACAGI ACACACACAGI ACACACACAGI ACACACACACAGI ACACACACACAGI ACACACACACACACACACACACACACACACACACACAC	KNITWITKEC! HBECADOII
				TTGTTTGGATATGTTGAAGAACACCAIGACIACAAAGGAAGIGIIIACAICGI	TAI BSGNKECPTCBKKI VS
				TTTGTGCAGACTGCATCATCACAGCCCTIAGAAGIGGCAACAAAAAAIGIC	KPSI BPDPNEDAI ISKIYPS
				CTACCTGTCGGAAAAAACIAGIIICCAAAAGAICACIAAGGCCAGAAAAAA	BOEVEAHOEBVI ABINKHN
				CTTTGATGCACTCATCAGCAAAATTIATCCAAGICGIGAIGAGIAIGAAGCIC	NOOAI SHSIEEGI KIOAMN
				ATCAAGAGAGTATTAGCCAGGATCAACAAGCACAATAATCAGCAAGAAGCACT	INCALS ISILECTING SAFD
				CAGTCACAGCATTGAGGAGGACTGAAGATACAGGCCATGAACAGACAG	NODESTICENIOEA
				GCGAGGCAAGAACAACAGATTGAAAATGGTAGTGGAGCAGAAGALAATGG	NGDSSHCSINASI HSINGEA
				TGACAGTTCACACTGCAGTAATGCATCCACACATAGCAATCAGGAAGCAGGC	ANIA AMAIDD WAD A SEIEL
				CCTAGTAACAAAGGACCAAAACATCTGATGATTCTGGGCTAGAGCTIGATA	NNAAMAIDE VINDGASEILL VEBBUBTI MEKDDSAOTBY
				ATAACAATGCAGCAATGGCAATIGAI CCAGIAAIGGAIGGIGCIACIAGIGAAAI	IKTSGNATVDHI SKYI AVBI
				TGAATTAGTATTCAGGCCTCATCCCACATTATGAAAAAAAA	ALEEL RSKGESNOMNLDTA
				CAGACGAGALACTO ACCOUNT CONTROL OF	SFKOYTIYIATASGOFTVLN
				GIAICI GIGCI GIGAGGI I AGONO ACTOR ACANACO I COMPAGO CANTANTA TANTANTA CONTRACTOR ACTOR AC	GSESI FI VSEKYWKVNKP
				AACCAGATGAACCTTGATACAGCCAGTGAGAAAGACAGTTTTTTTT	MELYYAPTKEHK*
	_			CAACAGCCAG GGCCAG I CACTGAACAAACCATGAACTTATTACGCAC	
				CTACAAAGGAGCACAAATGA	
Shigella	9	prey3596	186	ATGTCCAAGCGGCACCGGTTGGACCTAGGGGAGGATTACCCCTCTGGCAAG 387 AAGCGTGCGGGGACCGATGGGAAGGATCGAGATCGAGATCGAGATCGTGA	MSKRHRLDLGEDYPSGKK RAGTDGKDRDRDREDR
9.0				AGATCGGTCTAAAGATCGAGACCGAGAACGTGATAGAGGGAGATAGAGAGCG	SKDRDRERDRGDRERERE

TODASABY GLICION

999/Aud	187	GCTTA/TDASTGCTGGATTACA/CCCTGAAAGGTTCGCATT/CAACGGATTGA/CAACAACGATTGA/CAACAACGATTGA/CAACAACAACAACAACAACAACAACAACAACAACAACA	TWQXEF4UUEIQ	PHLAKASTASI TASARASTI TASARASTI TASARASTI TASARASTI SITASARASTI SI
999/aud		CGGACATCGAGGTCACACCTCACATTCCACAGGTCATTAATCGATATACCGATATACCGACAC TTACCCCATACCTCGATGATATTCTAAAGAAAACGTUTTCAGGTCCT TTACCCCATACCACCTCGATACTATGATATTCTAAAGAAAACGTUTTCAGGTCCT TTGTACATGATTGATAAACATGATATTCTGAGGTAGACACACAC	ZXEF4UUEIQ	GUNFT INTERT FAT DLA RLOLPWEYKDFFTDILG HGSFVLYGETGSGKTTGI HACVEYMRSLFGPKRGV CTGPRRAAMSVAGRVA CSSAKTFFWYMTGMLL ERMUNDFLERYGVIILDE REPTLATDILMGVLKEVYR BRSDLKVIVMSATLDA FRSI ESYHII RDGI EDPI F
999/Aud		THE SECRETATION CONTRIBUTION OF THE TABLES AND ADDRESS	TL 400TIG	HOSPY, VGET GSGKTTQI HROVEYMBSLPGPKRGV GTQPPRNAAMSVAGNVA GSSKKTFRWYMTOGML ERMINADLLENYGVIILDEA BRSDLKVIVMSATLDA RSDLKVIVMSATLDA
999/69U		TIGITICA DE CONTROCA CONTROCA CONTROCA DE	ADORIG	CTOPRINAAMSVAQHVA EMINVALGENGSVARTEF EGANNDPLLEHYGVIILDEA EETLATOILMGVLKEVVR RISDLKVNMSATLDA RISDLKVNMSATLDA
prey666		TACCAACCCAGGAGAGI GEG TEGAN IGAGA IN USOL CAGAGAT TOO DA TGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	OKIG	CSSAKTFFMYMTDGMLL IEAMNDPLLERYGVIILDEA IERTLATDILMGVLKEVVR IRSDLKVIVMSATLDA
prey666		GACTGCAGTAGTGCAAAAACATTTTTATGTATATGACTGATGGGATGTTACT TCGTGAAGCCTATGAATGATCCCCTCGAGGGGTTATGGTTAATATTCTTG ATGAGGCTGTAGAGGACACTGGCTACAGATATTCTAATGGGTGTTCTGAA ATGAGGCTACAAAAAAAAAA	ŒIO.	EAMNOPLLERYGVIILDEA IERTLATOILMGVLKEVVR RISOLKVIVMSATLDA ISSEI ESVHIII RDGI EDPI F
prey666		ATGAGGCTOTTGAGGGGGACACTGGCTACAGATATTCTAATGGTGTTTTGAA	8	RSDLKVIVMSATLDA
prey666				FOR ESVHIII RUGI FURI F
prey666		CTAGATGCAGG		T T T T T T T T T T T T T T T T T T T
		CATCACATCCCGGTTGGAATCTGTGCACATCATACTGAGAGATGGCCTGGAA 388		DTGI VOOOL DOLSTIGROE
		GA I CCCCI GGAGGAI ACGGGGC I GGI CCAGCAGCAGAI I CCAGCAGAGAI I CCACTCGTGCAGTTGT	<u> </u>	YEKTCALLVQLFDQSAQSY
		TTGACCAGTCGGCCCAGTCGTACCAGGAGCTGCTACAGAGCGCCAGCGCAA	Ų į	QELLQSASASPMDIAVQEG
		GCCCAATGGACATTGCAGTGCAGGAGGGAAGGCTGACATGGCTGGTTTACA	Ιø	RELIWEY IIGAVIGGEVSFA
		TTATTGGAGCAGTGATCGGI GGCCGGGIII		LMNLTDSRLAQAGNEKLEL
		AACAGATTCTCGTTTGGCCCAGGCGGGTAATGAGAAGCTAGAGTTGGCCAT	4 :	AMLSFFEQFRKIYIGDQVQ
	_	GCTGAGCTTTTTTGAACAGTTTCGTAAGATCTACATTGGGGACCAAGTGCAG	×	KSSKLYHH
	00.	AAATCCTCTAAGCTGTACCGCCGAAC		MTTLYTAKKYAVPALEAHC
prey3917	188	CCATTGCGTGGAGTTCCTGAAGAAGAACCTGCGAGCCGACAACGCCTTCAT		VEFLKKNLRADNAFMLLTQ
		GCTGCTCACGCAGGCGCGACTCTTCGATGAACCGCAGCTGGCCAGCCTGTG	Q.	ARLFDEPOLASLCLENIDKN
	_	CCTGGAGAACATCGACAAAAACACTGCAGACGCCATCACCGCGCGAGGGCTT		TADAII AEGE I DIDLDI LVA
		CACCGACATTGACCTGGACACGCTGGTGGCTGTCCIGGAGCGCGACACACI		WSEAFCOROOLOVTPENR
		GGGCALCCG1GAGG1GCGGC1G11CAA1GCCG11G1GCGC1GCCCAGGGGGGGG	. L	RKVLGKALGLIRFPLMTIEE
		TTCTGGGCAAGGCCCTGGGCCTCATTCGCTTCCCGCTCATGACCATCGAGG	_	FAAGPAQSGILVDREVVSL
		AGTTCGCTGCAGGTCCCGCACAGTCGGGCATCCTGGTGGACCGCGAGGTG		FLHFTVNPKPRVEFIDRPR
		GTCAGCCTCTTCCTGCACTTCACCGTCAACCCCAAGCCAAGGGAGTGAAGCGT	2 2	CCLHGKECSINHFOCVESH
		TTGACCGGCCCCGCTGCTGCGTGGGAAGGAGIGCAGCAICAACCGCI		WGTSGLSDRINI SVIKUIII
		TCCAGCAGGI GGAGAGI CGCI GGGGCI ACAGCGGGATTTGGGCTGTATGGAT	_	IQIIHTDSNTVLGQNDTGFS
		CCATCCACGGGCCCACCGACTACCAAGTGAACATCCAGATTATTCACACCGA		CDGSASTFRVMFKEPVEVL

TITEST DILLIG

				CHOCOCO	DVHOODDY ITACATVIANIA
			È.	TAGCAACACCGTCTTGGGCCAGAACGACACGGGCTTCAGCTGCGACGGCTC	TKGLRKYTHESPTTGAKTC
			¥ č	AGCCAGCACCI I CCGCG I CALGA I CAAAGAAGCCCAGACACCACACACACACACACACACACA	FTFCYAAGNNNGTSVEDG
_			<u> </u>	CALCAACIAAAAGGCCTGCGAAGGTGACACACGAGTCGCCCACCACGGGGCGCCA	QIPEVIFYT*
			Σĕċ	AGACCTGCTTCACCTTTTGCTACGCGGCCGGGAACAACAACAATGGCACATCCGT	
			\neg	GGAGGACGGCCAGAILCCCCGAGGICATOTTATTATTATTATTATTATTATTATTATTATTATTAT	CGKAFSWKSHLIEHORTHT
Shigella 7	prey63632		189		GEKPYHCTKCKKSFSRNSL
osbG			3 (CACACITICATE TO TRANSPORTED AND AN ATTICATED BOOK OF THE ANALYTICATED AND ATTICATED BOOK OF THE ANALYTICATED BOOK OF THE	LVEHQRIHTGERPHKCGEC
			Ĭ	TABATETETETETETETETETETETETETETETETETETE	GKAFRLSTYLIQHQKIHTGE
		_	- 4	ACCA A A A A TTC A CACT G G C G A G C C TTT C TTT G T A TTG A G C A A A A A TTC A C A C A C A C A C A C	KPFLCIECGKSFSRSSFLIE
			ζĂ	AGTITICAGICGGAGCICATTCCTTATTGAACATCAGAGGATCCATACTGGTG	HORIHTGERPYQCKECGK
		_	₹ ₹	AAAGACCTTATCAGTGCAAAGAGTGTGGGAAAAGTTTCAGTCAG	SFSQLCNLTRHORIHTGDK
			Ć	CCTTACTCGTCATCAGAGAATTCACACAGGAGACAAGCCCCATAAATGTGAG	PHKCEECGKAFSHSSGLIQ
) C	GAATGTGGAAAAGCCTTTAGTAGAAGCTCAGGTCTTATTCAGCATCAGAGAA	HORIHTHEKI YPYNEI KES
	_	_	5 ⊢	TTCACACCAGGGAGAAGACTTATCCATACAATGAAACTAAGGAAAGTTTTGAT	FDPNCSLVIQQEVYPKEKS
_		-	- C	CCAAATTGCAGTCTTGTTATACAGCAGGAAGTCTACCCTAAGGAGAAATCTTA	YKCDECGKTFSVSAHLVQH
		_	P	TAAATGTGAATGTGGGAAAACTTTTAGTGTTAGTGCTCATCTTGTACAAC	QRIHTGEKPYLCTVCGKSF
			4	ATCAAAGAATCCACACTGGTGAAAAGCCCTATCTATGTACTGTCTGT	SRSSFLIEHORIHT GERPYL
			נ פ	GAGCTTCAGCCGGAGCTCATTTCTTATTGAACATCAGAGAATCCACACTGGA	CROCGKSFSQLCNLIRHQG
			ט פ	GAGAGACCTATCTGTGCAGACAGTGTGGAAAAAGCTTTAGTCAGCTTTGTA	VHTGNKPHKCDECGKAFS
) ·d	ATCTATTCGACATCAGGGTGTTCACACAGGTAATAAACCCCATAAATGTGAT	RNSGLIQHQRIHTGEKPYK
	_		(C	GAATGTGGAAAGGCCTTTAGCCGGAACTCGGGTCTTATTCAGCATCAGAGAA	CEKCDKSFSQQRSLVNHQ
		_) -	TACACACAGAGAAAACCTTATAAGTGTGAGAAGTGCGACAAAAGTTTCAG	MIHAEVKTOETHECDACGE
			F	TCAACAGGGGAGTCTTGTCAACCATCAGATGATCCATGCAGAGGTGAAAACC	AFNCRISCIQHQKLHTAWM
	_		د د	CAAGAAACCCATGAATGTGATGCTTGTGGTGAAGCCTTTAATTGCCGTATTTC	*o
		_	_		MALIA IA SINONIANI I IGNE
Shidella 7	prev2109		190 G	GACTAAGGATCACCATTACTTTAAGTACTGCAAAATGICAGCAIIGGCICIIC	WALABSGONI EVAGE MI G
ospG			_	TGAAGATGGTGATGCCATGCCAGATCGGGAGGCAATTTATCOACAAGTGATTTTGC	KVDGETMIIMDSFALPVEGT
			<u>- </u>	TGATGCTAGGAAAGG GGA GG GAAACCATGA CATTA GGACAGTT GA TAT	FTBVNAQAAYEYMAAYIE
	_		_	GCC G GGAGGGCCCGAACCCGAACACACACACACACACACACAC	NAKOVGRI ENAIGWYHSH
			<u> </u>	GAATACATGGCTGCATACATAGAAAAIGCAAAACAGGIIGGCCGCCIIGAAA	PGYGCWI SGIDVSTOMLN
			⋖	ATGCAATCGGGTGGTATCATAGCCACCCTGGCTATGGCTGCTGCTGCTGTGTAG	COPPERAVIDETRISA
			ن	SATTGATGIIAGIACICAGAIGCICAAAICAGCAGIICCAAGAAAATATAAAAAAAAAA	GKVNI GAFBTYPKGYKPPD
				CAGTGGTGATTGATCCAACAACAACAATATCCGCAGGGAAAGGAACTTCT	EGPSEYOTIPLNKIEDFGVH
		_		CGCCT11AGGACA1ACCCAAAGGCTACAAAAAAAAAAAAA	CKOYYALEVSYFKSSLDRK
		_	٠. ن	GAGI ACCAGACIAI I COACI I AAI AAAA I AGAAGA I I I I COI COI COI COI COI COI COI COI	1
			_ (ACAALALIACCI I AGAAGI CI CAI AI I CAAALOO OO	
_	_	-	1	מכון מאפכו	

TODITUTEZ COLLICO

268	12/0/12/12/	394	GCTGGAGGATCTTCAGAAGAAG 395 MMASMRVVKELEDLUKKP CGATGATGCCAATGTCCTGGTG PPYLRNLSSDDANVLVWHA
			ATGATGGCGAGCATGCGAGTGGTGAAGGAGCTGGAGGATCTTCAGAAGAAG CCTCCCCCATACCTGCGGAACCTGTCCAGCGATGATGCCAATGTCCTGGTG
191	192	193	194
prey54201	prey1922	prey67418	prey67314
		_	7
Shigella ospG	Shigella ospG	Shigella ospG	Shigella

ACTUSAST DILIBR

				**************************************	PPEYPFKPPMIKFTTKIYHP
				ACCI GCGCA I CAGCI I CCCGCGGAGGIAI CONTROCO CONTROCO CAGCIA CONTROCO CAGCIA CAG	NVDENGQICLPIISSENWKP
				CTGCCCATCATCAGCAGTGAGAACTGGAAGCCTTGCACCAAGACTTGCAA	CTKTCGVLEALNVLVNKPNI
				GTCCTGGAGGCCCCCCGCAACTGGGGGAACTGCGAACTGCGAACTGCGGACTGGAACTGCGAACTGCGAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTAACT	RKNAEEFTLRFGVDRPS*
				AAGAATGCCGAAGAGIICACCCICCAAIICAGAAIIGGAACCAGACCAAI	MSVGHKAGESKIRYKTNEP
Shigella 7		prey67435	195		VWEENFTFFIHNPKRODLE
pdso				AGGACCTTGAAGTTGAGGTCAGAGACGAGCAGCACCAGTGTTCCCTGGGGA	VEVRDEQHQCSLGNLKVPL
_				ACCTGAAGGTCCCCTCAGCCAGGTGCTCACCAGTGAGGACATGACTGTGA	SQLLTSEDMTVSQRFQLSN
				GCCAGCGCTTCCAGCTCAGTAACTCGGGTCCAAACAGCACCATCAAGATGA	SGPNSTIKMKIALRVLHLEK
				AGATTGCCCTGCGGGTGCTCCATCTCGAAAAGCGAGAAAGGCCTCCAGACC	RERPPD
Chicollo 7		prev67443	196	CTGGGATGCCTCAAGGCTGCCGCCTATGCTGCTGAAGCCAACGACCACGA 397	WDALKAAAYAAEANDHELA
Ornigana Georgia		2000		GCTGGCCCAGGCCATCCTGGATGGAGCCAGCATCACCCTGCCTCATGGCAC	QAILDGASII LPHGI LCECY
D 0				CCTCTGTGAATGCTACGATGAGCTGGGCAATCGCTACCAGCTGCCCATCTAC	DELGNAYQLPIYCLSPPVN
				TGCCTGTCACCGCCGGTGAACCTGCTGCTGGAGCACACGGAGGAGGAGAG	CLLEHI EEESLEPPEPPSV
				CCTGGAGCCCCCCGAGCCTCCACCCAGCGTGCGCCCTGAGTTCCCGGCTGA	HREFPLKVRLSI GKDVRLS
	_			AGGTGCGCCTGTCCACGGCAAGGACGTGAGGCTCAGCGCCAGCCTGCCC	ASLPDTVGQLKHQLHAQE
				GACACAGTGGGGCAGCTCAAGAGGCAGCTGCACGCCCAGGAGGGCATCGA	GIEPSWORWFFSGNELLIUN
				GCCATCGTGGCAGCGGTGGTTCTTCTCCGGGAAGCTGCTCACAGACCGCAC	I ALGE I KIGKUFVIGVIIN
				ACGGCTCCAGGAGACCAAGATCCAGAAAGATTTTGTCATCCAGGTCATCATC	
		., 0.00	107	AAAC SOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	SVPSAARSSSAPSGCAPTS
Shigella 7	_	prey6/31/	'n.	CGICIEI GCCGICI GIGCCGCCACCACACACACACACACACACACACACACACA	KRCTGLPRRPWSSPVPST
osbg				TTTCATCATCAACCAGGCTTCTGCCTGGAACCTGGTGGGGGACATCCAGCAA	RASASWNLVGTSSKKLWG
				GAAGCTCTGGGGGACCAGCTACAGCTGGTGGAAGAGGAGTTTGCCCTCCAG	TSYSWWKRSLPSRA*
			_		***************************************
Shinella 7	1	prev67393	198	GAGAATCCACAAGGAATTGAATGATCTGGCACGGGACCCTCCAGCACAGTG 399	SELECTION OF THE SECOND SELECTION OF THE SECOND SEC
osnG OsnG				TTCAGCAGGTCCTGTTGGAGATGATATGTTCCATTGGCAAGCTACAATAATG	GPVGDDMFHWGAI IMGFIN
				GGGCCAAATGACAGTCCCTATCAGGGTGGAGTATTTTTCTTGACAALICALII	DSPTGGGVFFLINFIDI
			_	CCCAACAGATTACCCCTTCAAACCACCTAAGGTTGCATTTACAACAAGAAIII	PFKPFKVAFIIRITENING
-				ATCATCCAAATATTAACAGTAATGGCAGCATTTGTCTTGATATTCTACGATCA	NGSICLDILRSQWSPALI IS
				CAGTGGTCTCCAGCACTAACTATTTCAAAAGTACTCTTGTCCATCTGT1C1C1	KVLLSICSLLCDFNFDDFLV
				GTTGTGTGATCCCAATCCAGATGATCCTTTAGTGCCTGAGATTGCTCGGATC	PEIAHIYK I DHEKYNKIAKE
				TACAAAACAGATAGAGAAAAGTACAACAGAATAGCTCGGGAATGGACTCAGA	WICKAM
				AGTATGCGATGT AA	MOIOLO CACOLVINANBI PGW
Shigella 7	7	prey700	138	ATGGGAATTGGTCTTTCTGCTCAAGG IG I GAACA I GAA I AGAC ACCAGGT I 400 GGGATAAGCATTCGTTTTGTTCT	DKHSYGYHGDDGHSFCSS
				TCTGGAACTGGACAACCTTATGGACCAACTTTCACTACTGGTGATGTCALIG	GI GOPTGPITTI GDVIGCO

TODARADY RETAION

			GCTGTTGTGTTAATCTTATCAACAATACCTGCTTTTACACCAAGAATGGACAT	VNLINNTCFYTKNGHSLGIA FTDI PPNLYPTVGLQTPGE
			AGTITAGGTATIGCTITCACTGACCIACCGCCAATITGGGCACATCATTG GCTICAAACAGCAGGAGAGGGCAGCCAATITGGGCAACATCTTTG GCTICAAACAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	VVDANFGQHPFVFDIEDYM REWRTKIQAQIDRFPIGDR
			GIGITIGALAHARAKACIALAH ISCURGAAGGAGGAGGAGGAGAGACCAACGAATGGCGACCATGAT AGATAGATTCCTATCGGAGAATGGAGAAGGAGGAGGAGAATGGCGACCATGAT	EGEWOTMIOKMVSSYLVH
			ACAAAAATGGTTTCATCTTATTTAGTCCACCATGGGIACIGIGCCACACAGACAGAAAAAAATTGCCAGATCTACAGACCAGACCGTTCTAGAAGAATTAGCTTCCAT	EELASIKNRORIOKLVLAGR
			TAAGAATAGACAAAGAATTCAGAAATTGGTATTAGCAGGAAGAATGGGAGAA GCCATTGAAACAACAAAC	MGEAIETTQ
- 1	prey67411	200	GCCTGAAGAACAAGAAAAGAAAACCTTCTGCCACCAGCAGAAAAA 401	PEEQEERKPSATQQKKNT
			CACCAAACTCTCTAGCAAAACCACTGCTAAGTTATCCACTAGTGCTAATTGCAGTGC	LAEITLDPPPNCSAGPKGD
			TGGGCCTAAAGGAGATAACATTTATGAATGGAGATCAACTATACTTGGTCCA	NIYEWRSTILGPPGSVYEG
			CCGGGTTCTGTATATGAAGGTGGTGTTTTTTTTTCTGGATATCACATTTTCATC	GVFFLDITESSDYPFRPPRV
			AGATTATCCATTTAAGCCACCAAAGGTTACTTTCCGCACCAGAATCTATCACT	I KNWSPAI TISKVLLSICS
			GCAACATCAACAG CAGGGAG ICATCTGTCTGTCTATTTGTTGTTCCTTTTGA	LLTDCNPADPLVGSIATQYL
			CAGACTECAACCCTGCGGATCCTCTGGTTGGAAGCATAGCCACTCAGTATTT	TNRAEHDRIARGWTKRYAT
			GACCAACAGAGCAGAACACGACAGGATAGCCAGACAGTGGACCAAGAGATA	*
			CGCAACATAA	OS ISTAGED CABETEL SO
	prev67423	201	ATGAGTTCTCAACAGTTTCCTCGGTTAGGAGCCCCTTCTACCGGGCTGAGCC 402	MSSUCHFIEGALSI GLSC
			AGGCCCCTTCTCAGATTGCAAACAGTGGIICIGCIGGAIIGAIAAACCCAGG	NDESGROSEVSABEHMSS
			TGC ACAG CAA GA GAA CIGGGCGAAAA IOGAAAAIGAAGCAAGAAGCAAGAAGCAAGAAGAAGAAGAAGAAGAAG	SSSLOSREEKGEPVVVRPY
			CACATGAGTTCCAGCAGCICCCICCAGICCCGGGGAGGAAGGAAGCAAGAGCCI	POVOMLSTHHAVASATPVA
			GTTG1GG1AAGGCCCIAICCACAGG1GCAGATG1TG1CGACACACACGGGCACACGC	VTAPPAHLTPAVPLSFSEG
			COCA CARCACTATTCATTTCGGAGGACTTATGAAGCCGCCCCCGAAGC	LMKPPPKPTMPSRPIAPAP
			CCACCATGCCTAGCGTCCCATTGCTCCTGCTCCACCTTCTACCCTGTCACT	PSTLSLPPKVPGQVTVTME
			TCCCCCAAGGTTCCAGGGCAGGTTACCGTTACCATGGAGGAGTAGCATCCC	SSIPQASAIPVATISGQQGH
			TCAAGCTTCAGCCATTCCTGTGGCAACAATCAGTGGACAACAGGGGCCATCCC	PSNLHHIMI INVOMSIIRSN
			AGTAACCTGCATCACATCATGACTACAAATGTGCAAATGTCTATCATCGCAG	AFGFFERIGASHEF HGANA
			CAATGCTCCTGGGCCCCTCTTCACATTGGAGCTTCTCATTTACCTCGAGGT	DNIA ATAODAYOHIH
			GCAGCTGCTGCTGTGTGTGTCCAGTTCTAAAGTAACCACAGTCCTGAGGC	
			CGACCTCACAGCTGCCAAATGCTGCTACTCCTCAGCCAGC	
- 1	00000	Š	CALICACO	DILGVRVLQSPGTVLVDFIS
	preyo/298	Z/S	TATTICATGAGTGTGCATAAAACACCTTCTATCTATGGGACTGGCATGGGGC	*VCIKHLLSMGLAWGLVLXT
			TTGGTGCTTANAACATATAGATGAACAAGATCTTTGCTAGCAAGGAGCTGAG	PR'TRSLLARS'ELSEERVK
			AGCTTAGTGAAGAAGAGTGAAAAGI CCACAGI GAGAACAI GGAGGINGCAC	5

TOOTERS OFFICE

XPDPVLTLKNVXMIXRXG				MOPLSAPCTHINKWALL VTAGLINPWILPTTAGVTIE ACPRIVEGEXDVILLYHN PONLTGYWCGGIRDLYH VTSYVDGGIRICPAYSGSR FTAYSNAGGIRICPAYSGSR FTAYSNAGGIRICPAYSGSR FTAYSNAGGIRICPAYSGSR FTAYTHINGBOTRGVTG GSYTLHINGBOTRGVTG TSYCWWWINGGSLPWTHR TGOLSETHATLE-FGYNTYTA GPYECERINGSARSDP TJALLHGPDLPRIHPSYTNY RGSDNYTXGSRANSRPAQ YSWTINGKFGOSGONLFP COTTKHSGLYVGSVRNSAT GGESSTSLTVKVSASTRIGL IPLINFT
ATACCTGGGCTGCACTGCCTNTGCCTGATCCAGTCCTGACACTGA	AAAAN GUNIWA TURAN TAN SAGARAN GOOD AAAAN GU TARA GAAAA GU TARA GAAAA GU TARA GAAAAA GU TARA GAAAAA GU TARA GAAAAAA GU TARA GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TCAGTGCCTGCTAGATACTTTGACAAGTTGGCTAGAACAGGGTGTTCGAA GGAGCATTGAACACTCGAGATTACTTTCTTCACCATGGCAATTGATACTGAT GTTGCTTCCATCCTTAAGTACATTTACTTCTGAACTATGTATG	GIGTTGAGTATIOTOGGANNTNACGTT GCAATTGAGNUTCTGUTTGAGAAC CCTGAAAGAGTTUTCOCAGCTNAUGATNAGAGAGNOCGCTGGTGGGNOTO CCTGAAAGAGTTUTCOCAGCTNAUGATNAGAGAGNOCGCTGGTTTGCTT TTCCAACTACAANGAGGGCTTTGNNNNNTNTNCTATCAANGCGTGTTTTT TTCCAACTACAANNAGAGGGCTTTTGNNNNNTNTNCTATCAACTCTCTCCCGTTTTT TTCCAACTACAANTNCTTCTTGAGGANNNACTGGTTGTGNNGANGCNTNT ATANCCATCGAATTTGAAANGCNGAGNNNACGGTTGTGNNGANGCNTNT ATAGAANTTAGAAANGCNGAGNNNACGTGTTGTGNNGANGCNTNT	
	prey67464 203	prey67320 204	prey67321 205	prey35777 206
	7 pre	7 pq	7 pr	7
	Shigella ospG	Shigella ospG	Shigella ospG	Shigala ospG

IDDHS487.GIIIDE

			Ĭ	CTCCTTAATCCAACATAG	MOSSES CONTRACTOR
Shigella ospG	7	Ŀ	207	GAGGECTTT GACCOSTT TICT TO TRACEAST TO AGGGACCOCAN IN USE A 1995 GAGGAGECTT GACCOST TA TA GAGGAGT GAGGAGACCOCAN IN USE A 1995 GACCOGAGGAGT GAAN TO THE GAGGACAGAN TO AGGGACCOCTGAAGC GACCAGGAGAGAT TO THE TO GAGGACAGAGACT TO CAGGAGAGAGT TO THE CAGGAGAGAGAGAT TO THE TO CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	NSLDKRIVLAFRH.KLPTE NSLDKRIVLAFRH.KLPTE NWICGTOGALPAGERET LAMFAVRLGLERTWELL KRGGRRALSIHNOEGATPV SALE RGYHRIALOLITEEN AGEPDSWSSLSYEIPYGDC SYRHHRELDYTLTSESDS HHEHPFFGDGCTGPIFKLM NIOOQLMKTNLKOMDSLM NIOOQLMKTNLKOMDSLM REDGGFGFFRLM NIOOQLMKTNLKOMDSLM REDGGFGFFRLM NIOOQLMKTNLKOMDSLM REDGGFGFFRLM NIOOQLMKTNLKOMDSLM REDGGFGFFRLM NIOOQLMKTNLKOMDSLM REDGGFGFTDPOGTGFFRLM STGCCFGS TESTGCCFGS SAPKTTRYTYPAKAKGTFI
Shigella ospG		prey412	208		ADSHQNFALFFOLVDMNT AGAELTPHOTYNEHANGYG GEVVFVARPDNKNYVFEL DTSERKIEFDSASGTYTLYL IDDATLKNPILWNVADVNIK FPEELAPSTYLSONIFTPK GEIOHLFREPEKRPPT DATE OF THE OFFILE
Shigella ospG	2	prey50598	509	ACTOGNICATION CONTROLL AND THE ACTORNICATION CONTROLL AND	IGNISLLH VLSMOLOL YGE IGNISLLH VLSMOLOL YGE RRADGARAKEWRLHRGLSH RRASLEERAVSRNPLCTLC LEERRHPTATPCGHLFCW ECTRAWCSSRAECPLCREK FPPQKLIYLRHYRT INGTTUE!PDITNIACIE!
Shigella ospG	7	prey67364		TIATTAATGAAGAGAAGTATAAGAATA IAAGAGAAGAGA	AGENORHODI VEGPVCCL THTSRQVPRGRHHRPLR'G EALIEGETEAAHCLYLEVEN MXFCIYLC'LRXFTFXN SSKTAAKI STSAKRIOKELA
Shigella	7	prey67367	211	ATCCAGCAAAACCGCTGCTAAATTGTCAACTAGTGCTAAAAGAATTCAGAAAG	

					VIII OO TOO TOO TOO TELE
osbG				GAACTTGCAGAAATCACATTGGACCCTCCTCCCAACTGTAGTGCTGGACCCA AACGAGAAACATTATGAATGGAGGTCAACTATATTGGGACCCCCAGGATC	ENTLDPPPNCSAGPKGDNIY EWRSTILGPPGSVYEGGVF
				TATCTATGAGGGGGTGTTCTTGACATTACCTTTTCACCAGACTATC	FLDITESPDYPFKPPKVTFR
				CETTTA A A COCCOTA A GGTT A COTT COGA A CA A GA T CTAT CACT GTA A TAT	TRIYHCNINSQGVICLDILKD
				AACAGCCAAGGTGTGTGTCTGTCTGGACATCTTAAAGGACAACTGGAGTCCGG	NWSPALTISKVLLSICSLLI
				CTTTAACTATTTCTAAAGTTCTCCTCTCCATCTGCTCACTTCTTACAGATTGCA	DCNPADPLVGSIATQYMIN
				ACCCTGCTGACCCTCTGGTGGGCAGCATCGCCACACAGTACATGACCAACA	HAEHDHMAHQW I KHYAI
				GAGCAGAGCATGACCGGATGGCCAGACAGTGGACCAAGCGGTACGCCACA	
				TAG	VAMSRDGATHVYETHPWW
Shidella	7	prey67369	212	GTTGCAAIGAGCCGAGAIGGIGCCACICACICAIGIAIA	NEEDWOELDNI BSWKHSI
osoG				GGAACTTTTTCAGATGTGTGAGCICIGIAACCIIIIAAGGICCIGGAAATTAAAAATTAAAAATTAAAAAATTAAAAAATTAAAAA	EKSTI VISIBKI KI I AYIVISIK
				AGTATTTTAAAAGTACACTGTATAICICIAICAGGAAAIIAAAAIIGIIAGG	CKPYAMI IANI FNI I VIBI I B
				TATATCTACATTTCAATAAAATGTAAGCCIGIIGCIAIGIIGAIGAAGCAA	TCMNIM'*KEKIVETYI N
				TTTAACTTACTGGTCATTAGGCTGTTACGTACGTCAAIGAACIGGIGAAAGGA	SWILAW INCIN LINE
				GAAAATTTATGAAACATANCTCAAC	VINTRACOUNTAININININININININININININININININININI
ollogido	7	Draw67372	213	+=	DKVMSETNINFRCCMENT
Singalia	_				PRINT ASILDRIMADITO
osba				TTTAAATGTGTGTGGTGCTACACAGATTGGGAGAAAATCCCTTCCA	CGAANYTDWEKIPSMSKN
				TOTAGE A A COMPANY OF A STOCK OF A CONTRACT AND A CONTRACT OF A CONTRACT	RVPDSCCINVTVGCGINFN
				TO CARACK CONTROL OF THE CONTROL OF	EKAIHKEGCVEKIGGWLRK
				Index Inde	NVLVVAAAALGIAFVEVLGI
				TOO A ATTOCT THE TOO A SETTING THE SEA ATTOCT THE SECTION OF THE S	VFACCLVKSIRSGYEVM*
				GGGARII GCIII I GI CGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGAGGAG	
				-	XXXLNRHXLLXXTCKTXLX
Shigella		prey67379	214		XXATXGCXYXIXXXYWXLA
osbg				GNIGHTUNGGGCCACHAINNOC	HVKGXTVSXL*EXFLXC*XX
				NNNCINGEACHT TO TO TAKE THE ATTACK THE ATTACK TO THE ATTAC	STFHXISYXDVXYXNXXXX*
				IGNCCIGITAGNGTNAAAGTACTTTCACTNCACTTTCATNATGTATTTG	XHDXHSXCICHEXLIXXTCR
				LA INAGAACINGINININI LANTGINI GANTGAATAATAANACAATAAATAAATAAATAAATAAATAAATAA	NEN
		10000	1		MTVQALVEEVPMEINVKVF
Shigella	_	prey6/381	0		SKNOKENKFSPRKRREKY
osbe				CANANATATICAGGAAAACGGCTGCTAAATTGTCAACTAGTGCTAAAAGAATT	PAKPLLNCQLVLKEFRRNL
				CASAAGGAAGTTGCAGAAATCACATTGGACCCTCCTCCCAACTGTAGTGCTG	QKSHWTLLPTWVLDPKETT
			_	CACCOANAGE AGACATTTATGAATGGAGGTCAACTATATGGACCCCC	FMNGGQLYWDPQDLSMKE
			_	APPARTMENT TO THE ABORDED OF THE ACCUTATION OF	GCSFLTLPFHQTIRLNPLRL
				ACTATCCGTTTAAACCCCCTAAGGTTACCTTCCGAACAAGAATCTATCACTGT	PSEQESITVILTAKV*
				AATATTAACAGCCAAGGTGTGA	